

software version 5.1.1
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run sw model

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30 43.5 52.4 199 2 A41341
31 43.5 52.4 200 2 S17165
32 43.5 52.4 200 2 A41378
33 43.5 52.4 290 2 T21859
34 43.5 52.4 559 2 B42455
35 43 51.8 36 2 S12384
36 43 51.8 51 2 P10069
37 43 51.8 110 2 B34501
38 43 51.8 141 2 PS0147
39 43 51.8 171 1 HSUR15
40 43 51.8 203 2 F86145
41 43 51.8 206 2 SC9388
42 43 51.8 248 1 HSUR1P
43 43 51.8 249 2 T42339
44 43 51.8 285 2 S29368
45 43 51.8 286 2 AD1238

ALIGNMENTS

RESULT 1

histone H2B IV Volvox carterii

C:Species: Volvox carterii

C:Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #next_change 12-Feb-1993

C:Accession: JQ0797

R:Mueller, K.; Lindauer, A.; Brudekstein, M.; Schmitt, P.

Gene 93, 167-175, 1990

A:Title: Organization and transcription of Volvox carterii histone H2B IV gene

A:Reference number: JQ0794; M1019133024; F010122441

A:Accession: JQ0797

A:Molecule type: DNA

A:Residues: 1-155 <MUE>

A:Cross-references: GB:M31922; NCBI:J07657; F010122441; F010122441

A:Genetics:

A:Gene: H2B-IV

A:Superfamily: histone H2B

C:Keywords: chromosomal protein; DNA binding; nucleosome core; nucleos

Query Match 51.4% Score 51; DR 2; Length 155;

Best Local Similarity 69.2% Pred. No. 1.3;

Matches 9; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Cv 3 FFFHHHHHHHHHPS 10

Db 29 PFFHHHHHHHHHPS 41

RESULT 2

G88636

protein W09G12.7 (imported) - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 10-May-2001 #sequence_revision 10-May-2001 #next_change 10-May-2001

C:Accession: G88636

R:Anonymous, The C. elegans Sequencing Consortium.

Science 282, 2262-2269, 1998

A:Title: Genome sequence of the nematode C. elegans: A platform for investigating the

A:Reference number: A7500; M1019133024; F010122441

A:Note: See websites genome.washington.edu/ncbi/ and www.sanger.ac.uk/genomes/CELE/

A:Accession: G88636

A:Status: Preliminary

A:Molecule type: DNA

A:Residues: 1-368 <STO>

A:Cross-references: GB:J01417; F010122441; F010122441; F010122441

A:Genetics:

A:Gene: W09G12.7

A:Map position: 4

Query Match 61.4% Score 51; DR 2; Length 368;

Best Local Similarity 71.3% Pred. No. 1.7;

Matches 11; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

B: SASP-G - Bacillus subtilis (strain QMB1551) 111-kb pl
 revision 02 Dec 1994 #seq_change 16-Jul-1999
 v. 2.
 Sequence of a Bacillus subtilis gene coding for a minor sm
 09412497; PMID:9409242
 MIM:9304174; PMID:9304174; FID:9304175
 codon AAG for residue 115
 Soluble spore protein SASP is unusual in containing
 protein could be a component of Bacillus subtilis or Bacillus
 spore protein SASP
 storage protein
 the spore protein SASP - status experimental <MAT>
 Score 47; DB 1; Length 43;
 Prod. No. 3.9;
 Mismatches 3; Indels 0; Gaps 0;
 VISA: 12-Feb-1999 #seq_change 24-Jul-1999
 Odeh, M.; Schmitt, M.
 Triplication of VISA: 12-Feb-1999 #seq_change 24-Jul-1999
 9101024; PMID:9102411
 02-Feb-1999; PMID:9102411; FID:9102411
 DNA binding, nucleic acid binding, nucleus
 Score 47; DB 2; Length 177;
 Prod. No. 12;
 Mismatches 0; Indels 0; Gaps 0;
 Max. amino acids
 ter
 08-May-1999 #seq_change 05-Nov-1999
 Ireland, T.; Young, W.; Fothergill, A.L.; Graham, D.E.; O'

Nature 392, 353-358, 1998
 A:Title: The complete genome of the hyperthermophilic bacterium *Thermoplasma acidophilum*.
 A:Reference number: A70303; MIM:98196666; PMID:9530320
 A:Accession: C70474
 A>Status: Preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-422 <AOF>
 A:Cross-references: GB:AE000006, MIM:9424449; FID:AA000006; FID:9424449; TRAP:000006
 A:Experimental source: strain VF5
 C:Genetics:
 A:Gene: napA3
 Query Match
 Best Local Similarity 54.6%; Score 47; DB 2; Length 422
 Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0
 QY 3 PPKKKKKKKKK 13
 DB 301 PPKKKKKKKKK 301
 RESULT 11
 T21688
 Hypothetical protein F33A8.1 - *Caenorhabditis elegans*
 C:Species: *Caenorhabditis elegans*
 C:Date: 15-Oct-1993 #sequence_revision 15-Oct-1999 #seq_change 15 Oct 1999
 C:Accession: T21688
 R:Matthews, L.
 Submitted to the EMBL Data Library, November 1996
 A:Reference number: Z19459
 A:Accession: T21688
 A>Status: preliminary; translated from GB/EMBL/EBDC
 A:Molecule type: DNA
 A:Residues: 1-897 <WIL>
 A:Cross-references: EMBL:Z19459, FID:Z19459; GB:Z19459; FID:Z19459; TRAP:Z19459
 A:Experimental source: clone F33A8
 C:Genetics:
 A:Gene: CESP:F33A8.1
 A:Map position: 2
 A:Introns: 2a/2; 6/6; 9/9; 20/20; 21/21; 22/22; 23/23; 24/24; 25/25; 26/26; 27/27; 28/28; 29/29; 30/30
 Query Match
 Best Local Similarity 45.4%; Score 46; DB 2; Length 897
 Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0
 QY 3 PPKKKKKKKKK 15
 DB 736 PPKKKKKKKKK 746
 RESULT 12
 F84040
 Hypothetical protein BH3126 [imported] - *Bacillus halodurans* strain 7125
 C:Species: *Bacillus halodurans*
 C:Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #seq_change 16-Jun-2001
 C:Accession: F84040
 R:Takami, H.; Nakasone, Y.; Takaki, Y.; Maeda, G.; Sakaki, H.; Masui, N.; Fujii, E.; Hir
 Nucleic Acid Res. 28, 4317-4331, 2000
 A:Title: Complete genome sequence of the alkaliphilic bacterium *Bacillus halodurans* and
 A:Reference number: A83650; MIM:20512592; PMID:11059132
 A:Accession: F84040
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-67 <STO>
 A:Cross-references: GB:AP001517; GB:BA000004, MIM:31175509; FID:BA000004; FID:31175509
 A:Experimental source: strain C-125
 C:Genetics:
 A:Gene: BH3126
 Query Match
 Best Local Similarity 54.2%; Score 45; DB 2; Length 67;
 Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0

CY 3 PRKPKSPKSS 16
 1: |||||
 DB 45 PGNPKQPKSS 58

RESULT 13

T11744
 dehydrin kidney bean
 C:Species: Phaseolus vulgaris (L.) Hay 1966
 C:Date: 16-Jul-1996 #sequence_revision 16-Jul-1996 #ext_change 16-Jul-1996
 C:Accession: T11744
 R:Chai, T.Y., Burkard, G.
 submitted to the EMBL Data Library, April 1996
 A:Reference number: Z17392
 A:Accession: T11744
 A:Status: preliminary; translated from GR/EMBL/DBJ
 A:Molecule type: mRNA
 A:Size: 122 AAs
 A:Cross-references: EMBL:U54794, NID:gl59578
 A:Experimental source: Cultivar saka
 A:Note: regulated by dehydration stress, the heavy metal stress, and wounding
 C:Keywords: stress-induced protein

Query Match 54.2% Score 45; DP 2; Length 202;

Best Local Similarity 69.2% Pred. No. 29;

Matches 87; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

CY 1 DPKPKPKSPSK 13

1: |||||

DB 87 DPKPKPKSPSK 89

RESULT 14

A45317
 sperm-specific histone H1-like protein PL-11/PL-12 precursor, variant 1 North Pacific
 C:Species: Mytilus trossulus (North Pacific mussel)
 C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #ext_change 20-Sep-1999
 C:Accession: A45317
 R:Chai, T.Y., Burkard, G.
 submitted to the EMBL Data Library, April 1996
 A:Reference number: A45317; MUID:94107000; PMID:8416927
 A:Accession: A45317
 A:Molecule type: mRNA, protein
 A:Residues: 1-203 <CAR>
 A:Cross-references: GB:102875, NID:gl59578
 A:Note: sequence extracted from NCBI EMBL/GenBank/DBJ release 121301
 A:Note: this translation is not annotated in GenBank entry MSLHISTA, release 111.0
 C:Superfamily: histone H1
 C:Function: sperm-specific histone H1-like protein PL-11/PL-12 precursor, variant 1
 E146 203/1-203 sperm-specific histone H1-like protein PL-11/PL-12 precursor, variant 1

Query Match 54.2% Score 45; DP 2; Length 203;

Best Local Similarity 61.5% Pred. No. 29;

Matches 87; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

CY 3 PRKPKSPKSS 15

1: |||||

DB 185 PRKPKSPKSS 197

RESULT 15

T17250
 hypothetical protein DPKPKSPKSS 1 - human
 C:Species: Homo sapiens (man)
 C:Date: 18-Oct-1999 #sequence_revision 18-Oct-1999 #ext_change 18-Oct-1999
 C:Accession: T17250
 R:Kocher, E.; Beyer, A.; Mewes, H.W.; Gasteiger, S.; Wilmanns, S.
 submitted to the Protein Sequence Database, September 1999
 A:Reference number: Z18722
 A:Accession: T17250
 A:Status: preliminary

A:Molecule type: mRNA
 A:Residues: 1-482 <PRE>
 A:Cross-references: EMBL:AL117465
 A:Experimental source: adult uterus; clone DKFZps9610322
 C:Genetics:
 A:Note: DPKPKSPKSS 1

Query Match 54.2% Score 45; DP 2; Length 482;

Best Local Similarity 69.2% Pred. No. 61;

Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

CY 1 DPKPKPKSPKSS 15

1: |||||

DB 99 DPKPKPKSPKSS 106

Search completed: March 3, 2003, 06:35:25

Job time: 02:07:22 secs

Sequence verified (1993-2003) verified (1993-2003)

Sequence SW model

0. 615.03 / Search time 1.5954 Seconds
(with all updates)
Updating Multiple Cell Updates/sec

SPRINT 14

Input 0.5

4.17328 residues

01. Histon parameters 11.912

01

01

01. 1

01. 1

01. Results predicted by SW to have a total of the score 11.912, being printed, is of the total score 11.912.

SUMMARIES

Accession	Description
U00001	11958 volvox salt
U00002	11961 caenorhabditis
U00003	11967 xenopus lae
U00004	11971 homo sapien
U00005	11974 mus musculu
U00006	11977 volvox car
U00007	11986 rattus norv
U00008	11985 canis fami
U00009	11981 mytilus tro
U00010	11986 homo sapien
U00011	11992 bacillus su
U00012	11993 simad vito
U00013	11997 strongylo
U00014	11998 homo sapien
U00015	11999 cryptospor
U00016	12000 mus musculu
U00017	12001 homo sapien
U00018	12002 strongylo
U00019	12004 mus musculu
U00020	12007 echinocarpa
U00021	12008 paracanthus
U00022	12009 33-dia-
U00023	12010 mus musculu
U00024	12011 flatulib
U00025	12012 synchococ
U00026	12013 saetia
U00027	12014 equus cabd
U00028	12015 gallus gal
U00029	12016 homo sapien
U00030	12017 cricetus
U00031	12018 mus musculu
U00032	12019 sus scrofa
U00033	12020 sindbis vi

34	42.5	51.2	216	1	H1C1_XENLA
35	42	50.6	104	1	HMGC_MOUSE
36	42	50.6	109	1	HMGC_HUMAN
37	42	50.6	186	1	HMGC_HUMAN
38	42	50.6	213	1	HMGC_HUMAN
39	42	50.6	264	1	HMGC_HUMAN
40	42	50.6	268	1	HMGC_HUMAN
41	42	50.6	312	1	HMGC_HUMAN
42	42	50.6	344	1	HMGC_HUMAN
43	42	50.6	370	1	HMGC_HUMAN
44	42	50.6	377	1	HMGC_HUMAN
45	42	50.6	416	1	HMGC_HUMAN

ALIGNMENTS

RESULT 1
H2B4_VOLCA
ID H2B4_VOLCA STANDARD: PRT: 155 AA.
AC P16868; DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Histone H2B-IV.
OS Volvox carteri.
OC Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
OX Volvocaceae; Volvox.
OX NCBI_TaxID=3067;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN: Nagariensis / HK10;
FX MEDLINE accession: PubMed:222741;
RA Mueller K., Lindauer A., Bruderslein M., Schmitt P.;
RT "Organization and transcription of Volvox histone-encoding genes:
RT similarities between algal and animal genes.";
RL Gene 91:167-175(1990)
CC -!- SUBUNIT: THE NUCLEOSOME IS AN OLIGOMER CONTAINING TWO MOLECULES OF
CC H2A, H2B, H3, AND H4; WHICH WRAP APPROXIMATELY 140 BP OF DNA.
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- SIMILARITY: BELONGS TO THE HISTONE H2B FAMILY.
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CC or send an email to license@sib-sb.ch.
CC EMBL: M31922; AAA34250.1;
CC PIR: J00757; J00797;
CC InterPro: IPR000559; Histone H2B.
CC InterPro: IPR004822; Histone_core.
CC Pfam: PF00135; histone_1.
CC Rfam: RF00621; HISTONEH2B.
CC ProDom: PD000497; Histone_H2B; 1.
CC SWAPR: SMO0427; h2b; 1.
CC PROSITE: PS00157; HISTONE_H2B; 1.
CC NCBI: Protein; Chromosomal protein; Nucleosome core; H2B protein;
KW Multigene family.
JA SEQUENCE 155 AA. Total MW: 26430.77 kDa (P5940) (P5940)

Query Match: 01.48, Score 51.2, 100%, Length 155

Percent identity: 60.2%, Pct. Id. 0.861, Pct. Id. 0.861

Matches: 3, Conservative: 3, Mismatches: 1, Gaps: 0

Cy 3 PPKPKKSPKSS 15

|||||

Db 30 PPKPKKSPKSS 41

RESULT 2

us-09-214-913-37.rsp

Mon Mar 3 10:55:21 2003

DR EMBL: J00969; NOT_ANNOTATED_CDS.
 DR HSSP: P08287; 1GHC.
 DR InterPro: IPR001386; Histone_H1/H5.
 DR Pfam: PF00538; linker histone 1.
 DR ProDom: PD000173; LinkerHist_N; 1.
 DR SMART: SM0526; H1S;
 DR Chromosomal Protein; 6
 DR INTRON 0
 DR SEQUENCE 22616 MW, PR74CBB3A096186 CDS64;
 Query Match 59.0%; Score 49; DB 1; Length 200;
 Best Local Similarity 57.1%; Pred. No. 2.3; 2; Indels 0; Gaps 0;
 Matches 8; Conservative 4; Mismatches 0;
 QY 3 EYKYYKYYSPSKSSG 16
 Db 1: EYKYYKYYSPSKSSG 30
 RESULT 4
 ID 2148 HUMAN STANDARD; PRT; 794 AA.
 AC Q9UOR1; Q43591; C00389;
 DT 15-OCT-2001 (rel. 40, last sequence update)
 DT 15-OCT-2001 (rel. 40, last annotation update)
 DT 15-OCT-2001 (rel. 40, last annotation update)
 DT 15-OCT-2001 (rel. 40, last annotation update)
 DE Zinc finger protein 148 (Zinc finger DNA binding protein 89).
 DE (Transcription factor ZBP-89).
 GN ZNF148 OR ZBP89
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates, Catarrhini, Hominidae, Homo.
 OC Mammalia; Eutheria, Primates, Catarrhini, Hominidae, Homo.
 GX NCBI TaxID=9606;
 RN SEQUENCE FROM N.A. PubMed:19457682;
 RP MEDLINE:9457682; PubMed:19457682;
 RA Law D.J., Talle S.A., Morchut S.I.,
 KI "The human ZBP 89 homolog, located at chromosome 3p44, is a p160
 RT protein gene expression.";
 RL Mamm. Genome 9:165-167 (1998).
 EN SEQUENCE FROM N.A.
 RP MEDLINE:9285582; PubMed:10359087;
 RX Ye S., Whittington C., Watkins H., Henney A.,
 RA "Human stromelysin gene promoter activity is modulated by
 PT transcription factor ZBP-89.";
 RL PNAS Lett. 450:268-272 (1999).
 EN SEQUENCE FROM N.A.
 RP Law D.J., Chen X.N., Kornelius J.E., Morchut S.I., Morchut S.I.,
 RA "The growth-regulating transcription factor ZBP-89 is located at
 PT human chromosome 3p44 and mouse chromosome 8B1.";
 FL Submitted (Apr. 1999) to the EMBL/GenBank/DBP databases.
 CC - FUNCTION: INVOLVED IN TRANSCRIPTIONAL REGULATION. REVERSES THE
 CC - TRANSCRIPTION OF A NUMBER OF GENES INVOLVED IN THE PROLIFERATION OF
 CC AND ENLARGES. BINDS TO THE 3'-PICH BOX IN THE PROMOTER REGION OF
 CC THESE GENES.
 CC - SUBCELLULAR LOCATION: Nuclear.
 CC - SIMILARITY: BELONGS TO THE KRUEPPEL FAMILY OF C2H2-TYPE ZINC
 CC FINGER PROTEINS.
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 CC EMBL: AF039019; AAC039019.1;
 CC EMBL: A3236884; CAA15422.1;
 CC EMBL: U96633; AAB57692.1;
 CC HSSP: P08047; 1SP2.

Y0C2_CABE1 STANDARD; PRT; 346 AA.
 ID Y0C2_CABE1
 AC 01-NOV-1997 (rel. 35, last sequence update)
 DT 01-NOV-1997 (rel. 35, last sequence update)
 DT 01-NOV-1997 (rel. 35, last sequence update)
 DT 01-NOV-1997 (rel. 35, last sequence update)
 DE Hypothetical 39.2 kDa protein C12A2.1; in chromosome 11.
 GN C12A2.1
 OS Caenorhabditis elegans
 OC Eukaryota; Metazoa; Nematoda, Circularia, Phoronida; Rhabditidae;
 OC Rhabditidae; Rhabditidae; Caenorhabditis
 OC Rhabditidae; Rhabditidae; Caenorhabditis
 GX NCBI TaxID=6239;
 RN SEQUENCE FROM N.A.
 RP STRAIN=Bristol N2;
 RA Thomas K.;
 RA Submitted (Feb-1995) to the EMBL/GenBank/DBP databases.
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 CC EMBL: Z48241; CAA88295.1;
 CC WormBp: C12A2.1; C12A2.1;
 CC Hypothesis: protein;
 KW SEQUENCE 346 AA; 1922 MW; 5511204565092420 CDS64;
 Query Match 60.2%; Score 50; DB 1; Length 346;
 Best Local Similarity 50.0%; Pred. No. 2.6; 3; Indels 0; Gaps 0;
 Matches 9; Conservative 5; Mismatches 0;
 QY 1 DQKYYKYYSPSKSSG 15
 Db 4 DQKYYKYYSPSKSSG 18
 RESULT 3
 ID H2C2_XENLA STANDARD; PRT; 320 AA.
 AC H2C2_XENLA
 DT 01-APR-1996 (rel. 14, last sequence update)
 DT 01-APR-1996 (rel. 14, last sequence update)
 DT 01-APR-1996 (rel. 14, last sequence update)
 DT 01-APR-1996 (rel. 14, last sequence update)
 DE Histone H1C (Xenopus laevis)
 CC Xenopus laevis (Latin: X. laevis)
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Amphibia; Batrachia; Anura; Mesobatrachia; Pipiloidea; Pipiloidea;
 CC Xenodactylidae; Xenopus.
 GX NCBI TaxID=8455;
 RN SEQUENCE FROM N.A.
 RP MEDLINE:84555;
 RA Turner P.M., Aldridge J., Hirst G., Old K.W.;
 RA "Nucleotide sequences of H1 histone genes from Xenopus laevis. A
 RA recently diverged pair of H1 genes and an unusual H1 pseudogene.";
 RT Nucleic Acids Res. 11:4093-4107 (1983).
 RL Nucleic Acids Res. 11:4093-4107 (1983).
 CC - FUNCTION: HISTONE H1 ARE NECESSARY FOR THE CONDENSATION OF
 CC NUCLEOSOMES CHAINING INTO HIGHER ORDER STRUCTURES.
 CC - SUBCELLULAR LOCATION: Nuclear.
 CC - SIMILARITY: BELONGS TO THE HISTONE H1/H5 FAMILY.
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 CC EMBL: X01453; X01453.1;
 CC EMBL: X01453; X01453.1;
 CC EMBL: X01453; X01453.1;
 CC HSSP: P08047; 1SP2.

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Mon Mar 3 10:55:21 2003

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GN MLP OR MRP.
OS Oryctolagus cuniculus (Rabbit).
OT Eukaryota; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus
CX NCBI_TaxID:9986;
EN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
PC TISSUE:Macrophage;
RA MEDLINE:2038500; PubMed:1516135;
RT Li J., Adenem A.;
RT "MacMARCKS, a novel member of the MARCKS family of protein kinase C
RT substrates.";
RL Cell 70:791-801(1992).
CC -!- FUNCTION: MAY BE INVOLVED IN COUPLING THE PROTEIN KINASE C AND
CC -!- CALMODULIN SIGNAL TRANSDUCTION SYSTEMS.
CC -!- PTM: PHOSPHORYLATED.
CC -!- SIMILARITY: BELONGS TO THE MARCKS FAMILY.
CC -----
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CC -----
EMBL; S43921; AAB23156.1; -
DR PIR; A43341; A43341; MARCKS
DR InterPro; IFF02101; MARCKS
DR Pfam; PF02063; MARCKS; 1
DR PRINTS; PR00963; MARCKS.
DR PROSITE; PS00827; MARCKS.1; 1.
DR PROSITE; PS00827; MARCKS.2; 1
KW Phosphorylation; Myristate; Calmodulin-binding.
FT INIT_MET 0 0
FT LIPID 1 1 MYRISTATE (BY SIMILARITY).
FT DOMAIN 86 99 CALMODULIN BINDING (ESD). (BY SIMILARITY).
FT MOD_RES 92 92 PHOSPHORYLATION (BY PFC) (BY SIMILARITY).
FT MOD_RES 100 100 PHOSPHORYLATION (BY PFC) (BY SIMILARITY).
FT MOD_RES 103 103 PHOSPHORYLATION (BY PFC) (BY SIMILARITY).
SQ SEQUENCE 198 AA; 19635 MW; 6032A7E1E6D9CD4A CF754;

```

Query Match 52.4%; Score 43.5; DB 1; Length 198;
 Best Local Similarity 64.7%; Pred. No. 13; Indels 3; Gaps 1;
 Matches 11; Conservative 0; Mismatches 3;

Cy 3 FXXXXX XSPKSSG 16
 |||||
 D6 95 PXXXXXSPKPPPLSG 101

Search completed: March 3, 2003, 06:36:17
 Joo time : 24.6585 secs

102 particularly anti-angiogenic agents to
103 useful as wound treatment agents to
104 curatively promote epidermally fibrocytic
105 or epithelial growth in local treatment
106 of skin with, anti-infective prophylaxis, of
107 skin membranes which have a higher
108 pH than the eukaryotic organisms, also
109 membrane associated proteins, also
110 antimicrobial activity of an intravascular
111 agent the antibiotic resistant bacterial
112 represent peptides from in the
113

114 Score 13; DP 23; Conserved
115 Pred. No. 8,10-16;
116 Mismatches 0; Gaps 0;

AA

DT

117 "Fungal disease" is (10-16-16)
118 Central membrane protein, inflammation.

AA: PAB

119 Antibody Bounded to a specificity
120 and for treating a cancer related and
121 improved localization of cellular

AA

122 represents a specificity related membrane
123 relates to a soluble derivative (A) of a
124 a compound at least a heterologous
125 of low membrane affinity mutually
126 and independently and with homocysteine
127 cellular or artificial membranes ex vivo
128 are used to treat disorders treatable with
129 radiation or any other complement-related
130 disease, graft rejection, myocardial
131 arthritis and many others, including
132 cancer and thrombolytic disease, but also to
133 used to treat ischemic or ischemic and as
134 multiple sclerosis. A are administered

CC orally, topically, by injection or inhalation at 0.01-10 mg/kg/day.

XX Sequence 17 AA;

SQ Query Match

100.0%; Score 13; DP 16; Length 17;

Best Local Similarity 100.0%; Pred. No. 8,10-16;

Matches 16; Conservative 0; Mismatches 0; Gaps 0;

CY 1 DGPYKPKKPKKPKSSG 16

|||||

Db 1 DGPYKPKKPKKPKSSG 16

RESULT 5

AA: Y8862

ID AAY58862 standard; Peptide; 17 AA.

XX AC AAY58862;

XX DT 08-MAY-2000 (first entry)

XX DE Membrane binding element used in anti-angiogenic polypeptide.

XX KW Anti-angiogenic, angiogenesis inhibitor; membrane binding element;

XX KW cancer; tumor; therapy.

XX OS Synthetic.

XX FH Key Location/Qualifiers

XX FT Modified-site ; /note= "myristoylated"

XX PN WC200004052-A2.

XX PO 27-JAN-2000.

XX PF 16-JUL-1999; 99WO 0802292.

XX PR 16-JUL-1998; 98GB-0015505.

XX PA (ADPR-) ADPROTECH PLC.

XX PI Smith RAG, Bright JR, Steward M, Cox VF;

XX DR WPI; 2000-182406/16.

XX PT New soluble derivative of anti-angiogenic polypeptide useful for
XX treatment of primary or secondary cancer, including secondary related
XX membrane-binding elements for targeting
XX
XX Disclosure, Page 13; 36pp; English.

XX The present sequence is an example of a lysine-rich peptide

XX membrane binding element (MBE) that can be utilized in novel

XX soluble derivatives (A) of anti-angiogenic polypeptides of the

XX invention (A) consists of a heterologous MBE with low

XX membrane affinity that are covalently attached to a soluble

XX anti-angiogenic polypeptide such as a non-catalytic region of human

XX plasminogen, fragments of related proteins containing kinase

XX domains, fragments of collagen or prolactin, neutralizing

XX antibodies against receptors for angiogenic mediators, and

XX an array of binding involved in angiogenesis. The MBEs

XX interact independently with thermodynamic activity, with

XX components of the vascular endothelium. provide targeted

XX delivery of the anti-angiogenic polypeptide to cell membranes and

XX sites of active angiogenesis, particularly the vascular endothelium,

XX and therefore increase the local concentration and reduce the risk

XX of adverse effects on normal processes elsewhere in the vasculature.

XX They are used in a claimed method of treatment of primary or

XX secondary tumor.

XX Sequence 17 AA;

SQ

Query Match 100.0%, Score 83, DB 23, Length 17;
 Best Local Similarity 100.0%, Field No. 4.4e-05;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DGPFFKFKFKSPKSSG 16
 Df 1 DGPFFKFKFKSPKSSG 16

RESULT 6
 ABB07540
 ID ABB07540 standard, peptide; 88 AA.
 XX ABB07540;
 AC ABB07540;
 XX 23-APR-2002 (first entry)
 DE Amino acid sequence of APT2065

XX CCR9, lipid raft derivative; CAS; neuroprotective, neurotropic; human;
 XX cerebroprotective; antiparkinsonian; antiangiogenic; anticancer; cardiac;
 XX antidiabetic; antidiarrheal; dermatological; hypertensive; vasoprotective;
 XX antirheumatic; antiarthritic; antiinflammatory; ophthalmological;
 XX immunosuppressive; antiaugenic; nephroprotective; antiinfertility;
 XX antibacterial; antiatherosclerotic; vulnervary.

XX Synthetic.
 OS Homo sapiens.
 XX

PH Key Location/Qualifiers
 FT Disulfide bond 71-72 (note="disulphide bridge")
 FT
 XX WC000004638-A1.
 XX 17 JAN 2002.
 XX 06-JUL-2000; 2001WO 000034.
 XX 07 JUL 2000; 2000GB-0016811.
 XX (ADPR-) ADPROTECH LTD.
 XX Rowling RUE, Smith GP, Ridley SH;
 XX WPT: 2002-164645/21.

XX Lipid raft targeted derivative of a soluble polypeptide e.g. a soluble
 PT complement regulatory molecule for treating disorders involving
 PT complement activity and various inflammatory, neurological and immune
 PT disorders

XX Example 9, Page 47, Giff, English.

XX The invention relates to a soluble derivative (1) of a soluble
 CC polypeptide (2). It has two or more heterologous membrane binding elements
 CC with low membrane affinity covalently associated with the polypeptide.
 CC the elements being capable of interacting with components of cellular or
 CC artificial membranes exposed to extracellular fluids and target lipid
 CC raft components of membrane. It is useful for treating disorders
 CC associated with treatment by a soluble peptide fragment of CCR9, CCR5 or other
 CC chemokine receptors, and for the preparation of a reagent for treatment
 CC of disorders involving complement activity and various inflammatory and
 CC immune disorders. (1) is useful for treating neurological disorders (e.g.
 CC multiple sclerosis, stroke, Parkinson's, Alzheimer's disease, traumatic
 CC brain injury and allergic encephalitis), disorders of inappropriate or
 CC undesirable complement activation (e.g. xenograft rejection, neonatal
 CC jaundice, hemolytic transfusion reactions, including allergic transfu-
 CC sion reactions, hemolysis, hemolysis, hemolysis, hemolysis, acute
 CC pulmonary embolism, post-ischemic reperfusion conditions (e.g. myocardial
 CC infarction, hypotension, renal ischemia, necrosis, atherosclerosis),
 CC infection, bacterial meningitis (e.g. meningitis, meningitis, meningitis,
 CC infection, bacterial meningitis (e.g. meningitis, meningitis, meningitis,

CC shock), autoimmune diseases (e.g. rheumatoid arthritis, systemic lupus
 CC erythematosus, hemolytic anemia, glomerulonephritis and myeloma
 CC crisis), reproductive disorders (e.g. infertility), and wound healing.
 CC The present sequence represents the
 CC amino acid sequence of APT2065.

XX
 SQ Sequence 88 AA;
 Query Match 100.0%; Score 83; DB 23; Length 88;
 Best Local Similarity 100.0%; Field No. 4.4e-05;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DGPFFKFKFKSPKSSG 16
 Df 73 DGPFFKFKFKSPKSSG 88

RESULT 7
 ABB07538
 ID ABB07538 standard, peptide; 89 AA.
 XX ABB07538;
 AC ABB07538;
 XX 23-APR-2002 (first entry)
 DE Amino acid sequence of APT2062.

XX CCR9, lipid raft derivative; CAS; neuroprotective, neurotropic; human;
 XX cerebroprotective; antiparkinsonian; antiangiogenic; anticancer; cardiac;
 XX antidiabetic; antidiarrheal; dermatological; hypertensive; vasoprotective;
 XX antirheumatic; antiarthritic; antiinflammatory; ophthalmological;
 XX immunosuppressive; antiaugenic; nephroprotective; antiinfertility;
 XX antibacterial; antiatherosclerotic; vulnervary.

XX Synthetic.
 OS Homo sapiens.
 XX

PH Key Location/Qualifiers
 FT Disulfide bond 92-93
 FT
 XX WC000004638-A1.
 XX 17 JAN 2002.
 XX 06-JUL-2000; 2001WO 000034.
 XX 07 JUL 2000; 2000GB-0016811.
 XX (ADPR-) ADPROTECH LTD.
 XX Rowling RUE, Smith GP, Ridley SH;
 XX WPT: 2002-164645/21.

XX Lipid raft targeted derivative of a soluble polypeptide e.g. a soluble
 PT complement regulatory molecule for treating disorders involving
 PT complement activity and various inflammatory, neurological and immune
 PT disorders

XX Example 9, Page 46, Giff, English.

XX The invention relates to a soluble derivative (1) of a soluble
 CC polypeptide (2). It has two or more heterologous membrane binding elements
 CC with low membrane affinity covalently associated with the polypeptide.
 CC the elements being capable of interacting with components of cellular or
 CC artificial membranes exposed to extracellular fluids and target lipid
 CC raft components of membrane. It is useful for treating disorders
 CC associated with treatment by a soluble peptide fragment of CCR9, CCR5 or other
 CC chemokine receptors, and for the preparation of a reagent for treatment
 CC of disorders involving complement activity and various inflammatory and
 CC immune disorders. (1) is useful for treating neurological disorders (e.g.
 CC multiple sclerosis, stroke, Parkinson's, Alzheimer's disease, traumatic
 CC brain injury and allergic encephalitis), disorders of inappropriate or
 CC undesirable complement activation (e.g. xenograft rejection, neonatal
 CC jaundice, hemolytic transfusion reactions, including allergic transfu-
 CC sion reactions, hemolysis, hemolysis, hemolysis, hemolysis, acute
 CC pulmonary embolism, post-ischemic reperfusion conditions (e.g. myocardial
 CC infarction, hypotension, renal ischemia, necrosis, atherosclerosis),
 CC infection, bacterial meningitis (e.g. meningitis, meningitis, meningitis,

pharynx), disorders of inappropriate or excessive secretion of hormones, disorders (including obstructive colitis, diabetes, asthma, scleroderma, acute rejection conditions such as myocardial infarction, postoperative atherosclerosis, multiple organ failure, septic shock, rheumatoid arthritis, systemic lupus erythematosus, glomerulonephritis and vasculitis), antibody or complement mediated graft rejection, inflammatory diseases, Crohn's disease, uveitis, psoriasis, asthma, scleroderma, acute pancreatitis), post-ischaemic reperfusion conditions such as myocardial infarction, hypertension, renal ischaemia, testicular atrophy, arthritis, infectious diseases or sepsis (e.g. multiple organ failure), septic shock, autoimmune diseases (e.g. rheumatoid arthritis, systemic lupus erythematosus, haemolytic anemia, glomerulonephritis and myasthenia gravis), reproductive disorders, antibody or complement mediated infertility, and wound healing. The present sequence represents the amino acid sequence of APT2063.

Query Match 100.0%; Score 83; DP 13; Length 100
Best Local Similarity 100.0%; Pred. No. 58-75;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 1 DGPVYVYVYVSPVSSG 16
D6 95 DGPVYVYVYVSPVSSG 100
|||||

RESULT 9
AAW45898
ID AAW45898 standard; peptide; 214 AA.
XX
AC AAW45898;
XX
DT 30-JUN-1998 (first entry)
XX
DE SCR 1-3 of complement receptor type 1 (CD35) fused protein.
XX
KW Membrane binding element; thrombotic disease; soluble protein.
KW Complement related disease; integral membrane protein; inflammation.
KW Short consensus repeat; SCR 1-3; CRI; complement receptor type 1.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Cross-links 214
FT /note= "Disulphide linked to Cys 25 peptide, shown in AAW45898 or S-CH2-200NH-CH2-12H."

W09802454-A2.
XX
XX 22-JAN-1998.
XX
XX 08-JUL-1997; 97WC-EP03715.
XX
XX 15-JUN-1996; 96GP-0014871.
XX
XX (ADPR-) ADPPOTECH PLC.
XX
XX Ewli I. Mossakowska DE1, Smith RAG;
XX WFI; 1998-110524/10.
XX
XX Derivatives of soluble polypeptide's bonded to low affinity
PT membrane binding groups - useful for treating complement related and
PT thrombotic diseases, providing improved localisation at cellular
PT membranes
PS claim 22, Page 60, 76pp, English.
XX

artificial membranes exposed to extracellular fluids and a lipid raft component of membrane. It is useful for treating diseases amenable to treatment by a soluble peptide fragment of CD35, for other therapeutic agent and for the preparation of a medicament for treatment of disorders involving complement activity and various inflammatory and immune disorders. It is useful for treating neurological disorders such as multiple sclerosis, stroke, Parkinson's, Alzheimer's disease, traumatic brain injury and allergic encephalitis), disorders of inappropriate or undesirable complement activation (e.g. xenograft rejection, renal graft rejection, inflammatory diseases, Crohn's disease, uveitis, psoriasis, asthma, scleroderma, acute pancreatitis), post-ischaemic reperfusion conditions such as myocardial infarction, hypertension, renal ischaemia, testicular atrophy, arthritis, infectious diseases or sepsis (e.g. multiple organ failure), septic shock, autoimmune diseases (e.g. rheumatoid arthritis, systemic lupus erythematosus, haemolytic anemia, glomerulonephritis and myasthenia gravis), reproductive disorders, antibody or complement mediated infertility, and wound healing. The present sequence represents the amino acid sequence of APT2063.

Query Match 100.0%; Score 83; DP 13; Length 100
Best Local Similarity 100.0%; Pred. No. 58-75;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 1 DGPVYVYVYVSPVSSG 16
D6 95 DGPVYVYVYVSPVSSG 100
|||||

RESULT 9
AAW45898
ID AAW45898 standard; peptide; 214 AA.
XX
AC AAW45898;
XX
DT 30-JUN-1998 (first entry)
XX
DE SCR 1-3 of complement receptor type 1 (CD35) fused protein.
XX
KW Membrane binding element; thrombotic disease; soluble protein.
KW Complement related disease; integral membrane protein; inflammation.
KW Short consensus repeat; SCR 1-3; CRI; complement receptor type 1.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Cross-links 214
FT /note= "Disulphide linked to Cys 25 peptide, shown in AAW45898 or S-CH2-200NH-CH2-12H."

W09802454-A2.
XX
XX 22-JAN-1998.
XX
XX 08-JUL-1997; 97WC-EP03715.
XX
XX 15-JUN-1996; 96GP-0014871.
XX
XX (ADPR-) ADPPOTECH PLC.
XX
XX Ewli I. Mossakowska DE1, Smith RAG;
XX WFI; 1998-110524/10.
XX
XX Derivatives of soluble polypeptide's bonded to low affinity
PT membrane binding groups - useful for treating complement related and
PT thrombotic diseases, providing improved localisation at cellular
PT membranes
PS claim 22, Page 60, 76pp, English.
XX

CC This sequence represents a specifically cloned protein having the
 CC amino acid sequence of short consensus repeats (SCR 1A) of
 CC complement receptor type 1 (CR1) plus a switch fusion sequence. The
 CC invention relates to a soluble derivative (A) of a soluble polypeptide
 CC (B), which comprises at least 2 heterologous membrane binding elements
 CC (MBE) of low membrane affinity covalently associated with (U) MBE
 CC interact, independently and with thermodynamic additivity, with
 CC components of cellular or artificial membranes exposed to extracellular
 CC fluid. (A) are used to treat disorders treatable with (U) itself,
 CC specifically inflammation or any other complement-related disorder,
 CC to a non-lethal disease, graft rejection, mycobacterial infection,
 CC sepsis, rheumatoid arthritis and many others, including application to
 CC dialysis devices and thrombolytic disease, but also to treat allergy,
 CC induce weight loss, to treat ischaemia or asthma and to immunize
 CC a host to prevent multiple myeloma. (A) are administered orally,
 CC intrally, by injection or inhalation at a dose of preferably 0.1 to
 CC mg/kg/day.

SQ Sequence: 214 AA;

Query Match: 100.0%, Score 83, DB 19, Length 214,

Best local similarity: 100.0%, Seed NO. 000011;

Matches: 16; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

QV 1 DDPKFFKFFKSSSS 16

DB 199 DDPKFFKFFKSSSS 215

RESULT 10

AAW75997

10 AAW75997 standard, protein, 215 AA;

XX AAW75997;

18-JAN 1999 (first entry)

Complement receptor type 1-like polypeptide PM-9.

XX Complement receptor type 1, DB1, CM7, PM-9, complement inhibitor;
 XX myeloid leukaemia; soluble switch fusion protein; 1, 9W9P.1;
 XX anti-leukemic activity; anti-leukemic; anti-leukemic disease;
 XX xenograft rejection, inflammation, Crohn's disease, asthma;
 XX pancreatitis, post ischaemic reperfusion, infection, sepsis;
 XX autoimmune disease, rheumatoid arthritis; proliferative nephritis;
 XX myasthenia gravis; reproductive disorder; therapy.

XX Chimeric - Homo sapiens.

OS Chimeric - Synthetic.

XX Key Location/Qualifiers

PH Protein 1..197

FT Peptide /label= CM7

FT Peptide /label= MSWP-1

FT Disulfide-bond 198..199

FT Modified-site 199

FT Modified-site /note="(S 2 thiopyridyl)cysteine"

FT Modified-site 215

FT Modified-site /note="N (myristoyl) glycine"

XX W09819433-A1.

XX 11-SEP 1998.

XX 05-MAR-1999; 99W0-GR00127.

XX 05-MAR-1997; 97GB 004612.

XX 05-MAR-1997; 97GB 004612.

XX 05-MAR-1997; 97GB 004612.

XX 05-MAR-1997; 97GB 004612.

XX 05-MAR-1997; 97GB 004612.

XX 05-MAR-1997; 97GB 004612.

XX 05-MAR-1997; 97GB 004612.

XX 05-MAR-1997; 97GB 004612.

XX 05-MAR-1997; 97GB 004612.

XX 05-MAR-1997; 97GB 004612.

XX 05-MAR-1997; 97GB 004612.

WP, loop scores 43.

XX Soluble polypeptide comprising short consensus repeats from LHR-A
 XX used to treat disorders and diseases associated with inflammation or
 XX inappropriate complement activation

XX Claim 17; Page 52-53; 67pp; English.

XX This is the amino acid sequence of PM-9, a novel type 1-like
 XX complement receptor type 1-like polypeptide having a switch fusion
 XX sequence. The invention relates to a soluble derivative (A) of a soluble polypeptide
 XX (B), which comprises at least 2 heterologous membrane binding elements
 XX (MBE) of low membrane affinity covalently associated with (U) MBE
 XX interact, independently and with thermodynamic additivity, with
 XX components of cellular or artificial membranes exposed to extracellular
 XX fluid. (A) are used to treat disorders treatable with (U) itself,
 XX specifically inflammation or any other complement-related disorder,
 XX to a non-lethal disease, graft rejection, mycobacterial infection,
 XX sepsis, rheumatoid arthritis and many others, including application to
 XX dialysis devices and thrombolytic disease, but also to treat allergy,
 XX induce weight loss, to treat ischaemia or asthma and to immunize
 XX a host to prevent multiple myeloma. (A) are administered orally,
 XX intrally, by injection or inhalation at a dose of preferably 0.1 to
 XX mg/kg/day.

SQ Sequence: 215 AA;

Query Match: 100.0%, Score 83, DB 19, Length 215;

Best local similarity: 100.0%, Seed NO. 000011;

Matches: 16; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

QV 1 DDPKFFKFFKSSSS 16

DB 200 DDPKFFKFFKSSSS 215

RESULT 11

AAW75997

10 AAW75997 standard, protein, 215 AA;

XX AAW75997;

18-JAN 1999 (first entry)

Complement receptor type 1-like polypeptide.

XX Complement receptor type 1, DB1, CM7, PM-9, complement inhibitor;
 XX myeloid leukaemia; soluble switch fusion protein; 1, 9W9P.1;
 XX anti-leukemic activity; anti-leukemic; anti-leukemic disease;
 XX xenograft rejection, inflammation, Crohn's disease, asthma;
 XX pancreatitis, post ischaemic reperfusion, infection, sepsis;
 XX autoimmune disease, rheumatoid arthritis; proliferative nephritis;
 XX myasthenia gravis; reproductive disorder; therapy.

XX Chimeric - Homo sapiens.

OS Chimeric - Synthetic.

XX Key Location/Qualifiers

PH Protein 1..198

FT Peptide /label= CM15/cys

FT Peptide /label= MSWP-1

FT Disulfide-bond 198..199

FT Modified-site 199

FT Modified-site /note="(S 2 thiopyridyl)cysteine"

FT Modified-site 215

FT Modified-site /note="N (myristoyl) glycine"

XX W09819433-A1.

KW anti-infective; antiasthmatic; dermatological; hypertensive; vasospastic;
 KW anti-infective; antiasthmatic; anti-inflammatory; epidermatological;
 KW immunosuppressive; anti-anemic; refrigerant; antiferility;
 KW antibacterial; antithrombotic; vulnerary;
 XX
 XX Synthetic;
 OS Homo sapiens;
 XX
 XX Key Locating/Qualifiers
 FH Disulfide-bond 254..255
 FT Modified-site /note= "disulphide bridge"
 FT Modified-site 271
 FT /note "C terminal NH methyl"yl"
 XX
 XX W0200004619 A1.
 PH
 XX
 XX 17 JAN 2002.
 PD
 XX
 XX 06-JUL-2001; 2001WO-0503034.
 PF
 XX
 XX 07-JUL-2001; 2000SE-0018011.
 PR
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 XX (ADPR) ADPROTECH LTD.
 PA
 XX
 XX Rowling PUE, Smith GP, Ridley SH;
 PI
 XX
 XX WPI, 2001-10444-121.
 DE
 XX
 XX Lipid raft targeted derivative of a soluble polypeptide e.g. a soluble
 FT complement regulatory molecule for treating disorders involving
 FT complement activity and various inflammatory, neurological and immune
 PT disorders
 PT
 XX
 PS Claim 5; Page 48; 51pp; English.
 CC The invention relates to a soluble derivative (I) of a soluble
 CC polypeptide (II) has two or more heterologous membrane binding elements
 CC with low membrane affinity covalently associated with the polypeptide,
 CC the elements being capable of interacting with components of cellular or
 CC artificial membranes exposed to extracellular fluids and target lipid
 CC rich components of membrane. (I) is useful for treating disorders
 CC amenable to treatment by a soluble peptide fragment of CD59, DAF or other
 CC complement regulatory proteins, and (I) the preparation of a reagent for treatment
 CC of disorders involving complement activity and various inflammatory and
 CC immune disorders. (I) is useful for treating neurological disorders e.g.
 CC multiple sclerosis, stroke, Parkinson's, Alzheimer's disease, traumatic
 CC brain injury and allergic encephalitis; the therapy of ischaemic reperfusion
 CC undesirable complement activation (e.g. xenograft rejection, cerebral
 CC graft rejection), inflammatory disorders (including ulcerative colitis,
 CC Crohn's disease), uveitis, psoriasis, asthma, scleroderma, acute
 CC pancreatitis), post-ischaemic reperfusion conditions (e.g. myocardial
 CC infarction), hypertension, renal ischaemia, restenosis, other arteriosclerotic
 CC infectious diseases of sepsis (e.g. multiple organ failure, septic
 CC shock), autoimmune diseases (e.g. rheumatoid arthritis, systemic lupus
 CC erythematosus), haemolytic anaemia, glomerulonephritis and myasthenia
 CC gravis), reproductive disorders (infertility or spermicidal mediated
 CC infertility), and wound healing. The present sequence represents the
 CC amino acid sequence of A102334.
 XX
 SQ Sequence 271 AA;
 Query Match 100.0%; Score 83; DB 23; Length 271;
 Best Local Similarity 100.0%; Prod No 0 00014;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DDPKPKKPKSKSS 16
 DB 256 DDPKPKKPKSKSS 271
 |||||
 1 DDPKPKKPKSKSS 16
 |||||
 1 DDPKPKKPKSKSS 16
 RESULT 14
 AA045091
 1000 AA045091 standard; peptide, 16 AA.

XX AP045091;
 XX 1000000 (first entry)
 XX
 XX Peptide membrane binding element.
 XX
 XX Membrane binding element; thrombotic disease; inflammation;
 KW complement-related disease; soluble peptide.
 XX
 XX Synthetic.
 OS
 FH W00000454-A2.
 PH
 XX
 XX 22 JAN 1998.
 PD
 XX
 XX 09-JUL-1997; 97WO-EP03715.
 PF
 XX
 XX 15-JUL-1996; 96GR-0014871.
 PR
 XX
 XX (ADPR) ADPROTECH PLC.
 PA
 XX
 XX Dods J, Mossakowska DEI, Smith RAG;
 PI
 XX
 XX WPI, 1998-110524/10.
 DE
 XX
 XX Derivatives of cell-binding polypeptides linked to low affinity
 FT membrane binding groups - useful for treating complement-related and
 FT thrombotic diseases, providing improved localization at cellular
 PT membranes
 PT
 XX
 PS Claim 11, Page 70, 75pp, English.
 CC The present peptide sequence represents a specifically claimed membrane
 CC binding element. The invention relates to a soluble derivative (A) of a
 CC soluble polypeptide (I), which comprises at least 2 heterologous
 CC membrane-binding elements (MBE) of low membrane affinity covalently
 CC associated with (I). MBE interact, independently and with synergistic
 CC activity, with components of cellular and/or artificial membranes exposed
 CC to extracellular fluids. (A) are useful to treat disorders treatable with
 CC antibodies, specifically inflammation, e.g. the complement-related
 CC disorders (e.g. neurological disease, graft rejection, myocardial
 CC infarction, sepsis, the effects of arthritis and many others) including
 CC application to swelling reduction and shockolytic disease, but also to
 CC treatment of stroke, stroke weight loss, cerebral ischaemia or asthma and as
 CC immunomodulators for treating multiple sclerosis. (A) are administered
 CC orally, preferably by ingestion, at a dilution of 0.01 to preferably
 CC 0.1 to 10 mg/kg/day.
 XX
 XX Sequence 16 AA;
 Query Match 100.0%; Score 77; DB 19; Length 16;
 Best Local Similarity 100.0%; Prod No 0 10-05;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DDPKPKKPKSKSS 16
 DB 1 DDPKPKKPKSKSS 15
 |||||
 1 DDPKPKKPKSKSS 15
 |||||
 1 DDPKPKKPKSKSS 15
 RESULT 15
 AA058858
 1000000 standard; Peptide, 16 AA.
 ID AA058858
 XX
 XX AA058858;
 XX
 XX 08-MAY-2000 (first entry)
 DT
 XX
 XX Membrane binding element used in anti-angiogenic polypeptide.
 DE
 XX
 XX Anti-angiogenic, anti-thrombotic, fibrinolytic, membrane binding element;
 KW cancer; tumour; therapy.
 XX



Document released pursuant to
E.O. 13526

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[illegible]

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Model Parameters

• *For more information, contact:*

U.S. DEPARTMENT OF JUSTICE
FEDERAL BUREAU OF INVESTIGATION
WASHINGTON, D.C. 20535

[illegible]

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TABLE 1

[http://pubs.ccsenet.org/journal/view.php?id=7069](#)

Journal of Interpersonal Violence

results predicted by the model to have a positive effect on the score of the posttest being printed, and the total score distribution.

SAMPLES

Sequence 78, April
Sequence 150, A
Sequence 42813, A
Sequence 9, April
Sequence 9, April
Sequence 148, App
Sequence 517, App
Sequence 36617, A
Sequence 126683, A
Sequence 9, April
Sequence 18, April
Sequence 4, April
Sequence 3, April
Sequence 52, April
Sequence 702, App
Sequence 233, App
Sequence 261, App

41	49.4	59	US-09-925	29.9-39.9
20	41	61	US-09-926	29.9-39.9
21	41	61	US-09-927	29.9-39.9
22	41	61	US-09-928	29.9-39.9
23	41	90	US-09-929	29.9-39.9
24	41	147	US-09-930	29.9-39.9
25	41	154	US-09-931	29.9-39.9
26	41	219	US-09-932	29.9-39.9
27	41	278	US-09-933	29.9-39.9
28	41	316	US-09-934	29.9-39.9
29	41	378	US-09-935	29.9-39.9
30	41	378	US-09-936	29.9-39.9
31	41	378	US-09-937	29.9-39.9
32	41	378	US-09-938	29.9-39.9
33	41	378	US-09-939	29.9-39.9
34	41	378	US-09-940	29.9-39.9
35	41	378	US-09-941	29.9-39.9
36	41	378	US-09-942	29.9-39.9
37	41	530	US-09-943	29.9-39.9
38	41	645	US-09-944	29.9-39.9
39	41	923	US-09-945	29.9-39.9
40	41	1097	US-09-946	29.9-39.9
41	41	1388	US-09-947	29.9-39.9
42	40.5	42	US-09-948	29.9-39.9
43	40	482	US-09-949	29.9-39.9
44	40	482	US-09-950	29.9-39.9
45	40	482	US-09-951	29.9-39.9
46	40	482	US-09-952	29.9-39.9
47	40	482	US-09-953	29.9-39.9
48	40	482	US-09-954	29.9-39.9
49	40	482	US-09-955	29.9-39.9
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51	40	482	US-09-957	29.9-39.9
52	40	482	US-09-958	29.9-39.9
53	40	482	US-09-959	29.9-39.9
54	40	482	US-09-960	29.9-39.9
55	40	482	US-09-961	29.9-39.9
56	40	482	US-09-962	29.9-39.9
57	40	482	US-09-963	29.9-39.9
58	40	482	US-09-964	29.9-39.9
59	40	482	US-09-965	29.9-39.9
60	40	482	US-09-966	29.9-39.9
61	40	482	US-09-967	29.9-39.9
62	40	482	US-09-968	29.9-39.9
63	40	482	US-09-969	29.9-39.9
64	40	482	US-09-970	29.9-39.9
65	40	482	US-09-971	29.9-39.9
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67	40	482	US-09-973	29.9-39.9
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69	40	482	US-09-975	29.9-39.9
70	40	482	US-09-976	29.9-39.9
71	40	482	US-09-977	29.9-39.9
72	40	482	US-09-978	29.9-39.9
73	40	482	US-09-979	29.9-39.9
74	40	482	US-09-980	29.9-39.9
75	40	482	US-09-981	29.9-39.9
76	40	482	US-09-982	29.9-39.9
77	40	482	US-09-983	29.9-39.9
78	40	482	US-09-984	29.9-39.9
79	40	482	US-09-985	29.9-39.9
80	40	482	US-09-986	29.9-39.9
81	40	482	US-09-987	29.9-39.9
82	40	482	US-09-988	29.9-39.9
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86	40	482	US-09-992	29.9-39.9
87	40	482	US-09-993	29.9-39.9
88	40	482	US-09-994	29.9-39.9
89	40	482	US-09-995	29.9-39.9
90	40	482	US-09-996	29.9-39.9
91	40	482	US-09-997	29.9-39.9
92	40	482	US-09-998	29.9-39.9
93	40	482	US-09-999	29.9-39.9
94	40	482	US-09-1000	

ALIGNMENTS

```

1  RESULT 1
2  TS-09-905-301.78
3  Applicant: Smith, Louis C.
4  Applicant: Sparrow, James T.
5  Applicant: Hauer, Jocheb
6  Applicant: Mims, Martha P.
7  TITLE OF INVENTION: LIPOPHILIC PEPTIDES FOR
8  MACROMOLECULE DELIVERY
9  NUMBER OF SEQUENCES: 129
10  CORRESPONDENCE ADDRESS:
11  ADDRESSEE: LYCIN & LYCIN
12  STREET: 633 West Fifth Street
13  CITY: Suite 4700
14  CITY: Los Angeles
15  STATE: California
16  COUNTRY: U.S.A.
17  ZIP: 90071-2066
18  COMPUTER READABLE FORM:
19  MEDIUM TYPE: 3.5" Diskette, 1.44 Mb.
20  COMPUTER: IBM Compatible
21  OPERATING SYSTEM: IBM P.C. DOS 4.0
22  SOFTWARE: Word Perfect 6.1
23  CURRENT APPLICATION DATA:
24  APPLICATION NUMBER: US/90/065,301
25  FILING DATE: 11 Mar 2001
26  CLASSIFICATION: <Unknown>
27  PRIOR APPLICATION DATA:
28  APPLICATION NUMBER: 08/594,043
29  FILING DATE: <Unknown>
30  ATTORNEY/AGENT INFORMATION:
31  NAME: Warburg, Richard J.
32  REGISTRATION NUMBER: 40,427
33  REFERENCE/DOCKET NUMBER: 217189
34  TELECOMMUNICATION INFORMATION:
35  TELEPHONE: (213) 489-1600
36  TELEFAX: (213) 955-0440
37  TELEX: 67-3510
38  INFORMATION FOR SERIAL 78:

```

us-09-214-913-37.rapb

Mon Mar 3 10:55:20 2003

```

SEQUENCE CHARACTERISTICS:
  LENGTH: 17 amino acids
  TYPE: amino acid
  STRANDEDNESS: single
  TOPOLOGY: linear
  MOLECULAR TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 78
US-09-864-864 78

Query Match          55.4%; Score 46; DB 9; Length 17;
Best Local Similarity 72.1%; Pred. No. 53;
Matches          8; Conservative          0; Mismatches          1; Indels          0; Gaps          0;

QY 3 PNYKYYKPSK 14
DB 4 PNYKYYKPSK 15

RESULT 2
US-09-764-864 1122
Sequence 1122, Application US/09/764/864
Patent No. US2002012753A1
GENERAL INFORMATION
  APPLICANT: Posen et al
  TITLE OF INVENTION: Purloin Acids, Proteins, and Antibodies
  FILE REFERENCE: PT223
  CURRENT APPLICATION NUMBER: US/09/764/864
  Prior application data removed - consult PALM or file wrapper
  NUMBER OF SEQ ID NOS: 1792
  SOFTWARE: PatentIn Ver. 2.0
  SEQ ID NO 1122
  FEAT: 4aa
  TYPE: PPT
  ORGANISM: Homo sapiens
  FEATURE: NAME/KEY: CITE
  LOCATION: 6
  OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-864 1122

Query Match          55.4%; Score 46; DB 10; Length 499;
Best Local Similarity 72.1%; Pred. No. 53;
Matches          8; Conservative          2; Mismatches          1; Indels          0; Gaps          0;

QY 3 PNYKYYKPSK 13
DB 22 PNYKYYKPSK 232

RESULT 3
US-09-864-761-42813
Sequence 42813, Application US/09/864/761
Patent No. US2002048763A1
GENERAL INFORMATION
  APPLICANT: Posen, Charron G.
  APPLICANT: Rank, David P.
  APPLICANT: Hanzel, David K.
  APPLICANT: Chao, Wensheng
  TITLE OF INVENTION: HUMAN ANTI-CD44 SINGLE DOMAIN ANTIBODY ACID EPITOPES USEFUL FOR
  TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
  FILE REFERENCE: America X-1
  CURRENT APPLICATION NUMBER: US/09/864/761
  CURRENT FILING DATE: 2001-05-23
  PRIOR APPLICATION NUMBER: US 60/180,312
  PRIOR FILING DATE: 2000-02-04
  PRIOR APPLICATION NUMBER: US 60/207,456
  PRIOR FILING DATE: 2000-05-26
  PRIOR APPLICATION NUMBER: US 60/612,366
  PRIOR FILING DATE: 2000-04-03
  PRIOR APPLICATION NUMBER: GB 24263.6
  PRIOR FILING DATE: 2000-10-04
  PRIOR APPLICATION NUMBER: US 60/236,359

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PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,587
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 60/234,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 60/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
SEQ ID NO 42813
LENGTH: 64
TYPE: PPT
ORGANISM: Homo sapiens
FEATURE:
  OTHER INFORMATION: MAP TO AL035703.17
  OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.1
  OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1
  OTHER INFORMATION: EXPRESSED IN B14.4, SIGNAL = 1.5
  OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.1
  OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.2
  OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.1
  OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.2
  OTHER INFORMATION: EST HUMAN HIT: BF64974.2, EVALUATE 3.00E-21
  OTHER INFORMATION: SWISSPROT HIT: P18711, EVALUATE 1.50E-02
US-09-864-761 42813

Query Match          54.2%; Score 45; DB 10; Length 68;
Best Local Similarity 72.7%; Pred. No. 12;
Matches          1; Conservative          1; Mismatches          0; Indels          0; Gaps          0;

QY 1 DGRVYKPSK 11
DB 44 DGRVYKPSK 54

RESULT 4
US-10-060-763-9
Sequence 9, Application US/10/060/763
Publication No. US200202286A1
GENERAL INFORMATION
  APPLICANT: Currie, Barry A.J.
  TITLE OF INVENTION: B-193
  FILE REFERENCE: 10147-A
  CURRENT APPLICATION NUMBER: US/10/060/763
  CURRENT FILING DATE: 2002-01-10
  NUMBER OF SEQ ID NOS: 12
  SOFTWARE: PatentIn Ver. 2.0
  SEQ ID NO 9
  LENGTH: 709
  TYPE: PPT
  ORGANISM: Homo sapiens
US-10-060-763-9

```



```

; APPLICANT: Coler, Rhea
; APPLICANT: Probst, Peter
; APPLICANT: Brannon, Mark
; TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USE IN THE
; TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF LEISHMANIASIS
; FILE REFERENCE: 210121.42008
; CURRENT APPLICATION NUMBER: US/07/54,123
; CURRENT FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 732
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-874-923-18

```

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Query Match 51.88; Score 43; DB 10; Length 732;
Best Local Similarity 69.28; Pred. No. 3.1e-02;
Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

CY 1 DGPYKPYKPYKPYK 13
DB 271 DGPYKPYKPYKPYK 293

RESULT 14
US-09-982-091A-4
; Sequence 4, Application US/02/0982-091A
; Patent No. US20020151030A1
; GENERAL INFORMATION:
; APPLICANT: CALIFORNIA INSTITUTE OF TECHNOLOGY
; APPLICANT: KUMAGAI, Akiro
; APPLICANT: DUNPHY, William
; TITLE OF INVENTION: CLASSIN FACILITING AND METHODS OF USE HEREOF
; FILE REFERENCE: CIT3320-1
; CURRENT APPLICATION NUMBER: US/04/982,091A
; CURRENT FILING DATE: 2002-10-17
; PRIOR APPLICATION NUMBER: US 66/241,246
; PRIOR FILING DATE: 2000-10-17
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 1332
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-982-091A-4

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Query Match 51.88; Score 43; DB 10; Length 1332;
Best Local Similarity 69.28; Pred. No. 3.1e-02;
Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

CY 4 KPYKPYKPYKPYK 14
DB 245 KPYKPYKPYKPYK 257

RESULT 15
US-10-071-900-3
; Sequence 3, Application US/10071900
; Patent No. US20020127541A1
; GENERAL INFORMATION:
; APPLICANT: St. George-Hyslop, Peter H.
; APPLICANT: Rommens, Johanna
; APPLICANT: Fraser, Paul E.
; TITLE OF INVENTION: Alzheimer's Related Proteins and Methods
; TITLE OF INVENTION: OF USE
; FILE REFERENCE: 1034/1810-091
; CURRENT APPLICATION NUMBER: US/10/071,900
; CURRENT FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US/09/227,725
; PRIOR FILING DATE: 1999-01-08
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 3.0

```

```

; APPLICANT: Coler, Rhea
; APPLICANT: Probst, Peter
; APPLICANT: Brannon, Mark
; TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USE IN THE
; TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF LEISHMANIASIS
; FILE REFERENCE: 210121.42008
; CURRENT APPLICATION NUMBER: US/07/54,123
; CURRENT FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 732
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-874-923-18

```

```

Query Match 51.88; Score 43; DB 10; Length 732;
Best Local Similarity 69.28; Pred. No. 3.1e-02;
Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

CY 1 DGPYKPYKPYKPYK 13
DB 271 DGPYKPYKPYKPYK 293

RESULT 14
US-09-982-091A-4
; Sequence 4, Application US/02/0982-091A
; Patent No. US20020151030A1
; GENERAL INFORMATION:
; APPLICANT: CALIFORNIA INSTITUTE OF TECHNOLOGY
; APPLICANT: KUMAGAI, Akiro
; APPLICANT: DUNPHY, William
; TITLE OF INVENTION: CLASSIN FACILITING AND METHODS OF USE HEREOF
; FILE REFERENCE: CIT3320-1
; CURRENT APPLICATION NUMBER: US/04/982,091A
; CURRENT FILING DATE: 2002-10-17
; PRIOR APPLICATION NUMBER: US 66/241,246
; PRIOR FILING DATE: 2000-10-17
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 1332
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-982-091A-4

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Query Match 51.88; Score 43; DB 10; Length 1332;
Best Local Similarity 69.28; Pred. No. 3.1e-02;
Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

CY 4 KPYKPYKPYKPYK 14
DB 245 KPYKPYKPYKPYK 257

RESULT 15
US-10-071-900-3
; Sequence 3, Application US/10071900
; Patent No. US20020127541A1
; GENERAL INFORMATION:
; APPLICANT: St. George-Hyslop, Peter H.
; APPLICANT: Rommens, Johanna
; APPLICANT: Fraser, Paul E.
; TITLE OF INVENTION: Alzheimer's Related Proteins and Methods
; TITLE OF INVENTION: OF USE
; FILE REFERENCE: 1034/1810-091
; CURRENT APPLICATION NUMBER: US/10/071,900
; CURRENT FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US/09/227,725
; PRIOR FILING DATE: 1999-01-08
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 3.0

```

```

; APPLICANT: Coler, Rhea
; APPLICANT: Probst, Peter
; APPLICANT: Brannon, Mark
; TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USE IN THE
; TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF LEISHMANIASIS
; FILE REFERENCE: 210121.42008
; CURRENT APPLICATION NUMBER: US/07/54,123
; CURRENT FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 732
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-874-923-18

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Query Match 51.88; Score 43; DB 10; Length 732;
Best Local Similarity 69.28; Pred. No. 3.1e-02;
Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

CY 1 DGPYKPYKPYKPYK 13
DB 271 DGPYKPYKPYKPYK 293

RESULT 14
US-09-982-091A-4
; Sequence 4, Application US/02/0982-091A
; Patent No. US20020151030A1
; GENERAL INFORMATION:
; APPLICANT: CALIFORNIA INSTITUTE OF TECHNOLOGY
; APPLICANT: KUMAGAI, Akiro
; APPLICANT: DUNPHY, William
; TITLE OF INVENTION: CLASSIN FACILITING AND METHODS OF USE HEREOF
; FILE REFERENCE: CIT3320-1
; CURRENT APPLICATION NUMBER: US/04/982,091A
; CURRENT FILING DATE: 2002-10-17
; PRIOR APPLICATION NUMBER: US 66/241,246
; PRIOR FILING DATE: 2000-10-17
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 1332
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-982-091A-4

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Query Match 51.88; Score 43; DB 10; Length 1332;
Best Local Similarity 69.28; Pred. No. 3.1e-02;
Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

CY 4 KPYKPYKPYKPYK 14
DB 245 KPYKPYKPYKPYK 257

RESULT 15
US-10-071-900-3
; Sequence 3, Application US/10071900
; Patent No. US20020127541A1
; GENERAL INFORMATION:
; APPLICANT: St. George-Hyslop, Peter H.
; APPLICANT: Rommens, Johanna
; APPLICANT: Fraser, Paul E.
; TITLE OF INVENTION: Alzheimer's Related Proteins and Methods
; TITLE OF INVENTION: OF USE
; FILE REFERENCE: 1034/1810-091
; CURRENT APPLICATION NUMBER: US/10/071,900
; CURRENT FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US/09/227,725
; PRIOR FILING DATE: 1999-01-08
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 3.0

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; SEQ ID NO 3
; LENGTH: 1084
; TYPE: PRT
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (115)
; OTHER INFORMATION: Xaa can be any amino acid
US-10-071-900-3

Query Match      50.6%; Score 42; DP 12; Length 1084;
Best Local Similarity 60.0%; Pred. No. 3.5e+02;
Matches 2; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

2Y  2 GPRVYVYVSPKSSG 16
   | | | | | | | |
Db  663 GPRVYVYVSPKSSG 683

Search Completed: March 3, 2003, 06:41:38
Job time : 48.0244 secs

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; FILING DATE: 19-JUN-1985
 ; APPLICATION NUMBER: 627,811
 ; FILING DATE: 05-JUL-1984
 ; DEC 10 NO.2.
 ; LENGTH: 142
 5492709-2

Query Match 55.43, Score 46.5, DB 6, Length 242;

Best Local Similarity 52.43, Pred. No. 8.7, Matches 11; Conservative 2, Mismatches 2, Indels 5, Gaps 1,

QY 1 DGPFFKKK-----SPSKSS 16
 : ||||| :
 Db 104 EGTGKKKKKKGGGKSS 124

RESULT 3
 US-08-584-043A-78
 ; Sequence 78, Application US/08584043A
 ; Patent No. 6344436
 ; GENERAL INFORMATION:
 ; APPLICANT: Smith, Louis C.
 ; APPLICANT: Sparrow, James F.
 ; APPLICANT: Hauer, Gochen
 ; APPLICANT: Mins, Martha F.
 ; TITLE OF INVENTION: LIPOPHILIC PEPTIDES FOR
 ; TITLE OF INVENTION: LIPOPHILIC PEPTIDES FOR
 ; NUMBER OF SEQUENCES: 133
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Lyon & Lyon
 ; STREET: 633 West Fifth Street
 ; CITY: Los Angeles
 ; STATE: California
 ; COUNTRY: U.S.A.
 ; ZIP: 90071-2066
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 3.5" Diskette, 1.44 MB
 ; MEDIUM TYPE: 3.5" Diskette, 1.44 MB
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: IBM PC DOS 6.0
 ; SOFTWARE: Word Perfect 6.1
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/584,043A
 ; FILING DATE: January 9, 1992
 ; CLASSIFICATION: 437
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER:
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Warburg, Richard J.
 ; REGISTRATION NUMBER: 11,327
 ; REFERENCE/DOCKET NUMBER: 217/189
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (213) 483-1696
 ; TELEFAX: (213) 955-0440
 ; TELEX: 67-3516
 ; INFORMATION FOR SEQ. NO. 78:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 17 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: Peptide
 US-08-584-043A-78

Query Match 55.43, Score 46, DB 4, Length 17,

Best Local Similarity 76.9%, Pred. No. 0.76, Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 PKKKKKSPSKS 14
 : ||||| :
 Db 4 PPKSPKSPSKS 15

RESULT 4

US 08 492 085P-20
 ; Sequence 20, Application US/08492085P
 ; Patent No. 6018030
 ; GENERAL INFORMATION:
 ; APPLICANT: Petrati, Franco A.
 ; APPLICANT: Richardson, Charles
 ; APPLICANT: Chambers, James
 ; APPLICANT: Causey, Stuart
 ; APPLICANT: Pollock, Thomas J.
 ; APPLICANT: Caspell, Joseph
 ; APPLICANT: Crissman, John W.
 ; TITLE OF INVENTION: N-Substituted Peptides Containing Epitopes
 ; TITLE OF INVENTION: N-Substituted Peptides Containing Epitopes
 ; NUMBER OF SEQUENCES: 112
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
 ; STREET: Four Embarcadero Center, Suite 3400
 ; CITY: San Francisco
 ; STATE: California
 ; COUNTRY: US
 ; ZIP: 94111
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC DOS/MS DOS
 ; SOFTWARE: Patent Plus #1.0, Version #1.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/492,085B
 ; FILING DATE: 07-JUN-1995
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 06/927,258
 ; FILING DATE: 04 NOV-1986
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/114,618
 ; FILING DATE: 29-OCT-1987
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 06/053,849
 ; FILING DATE: 22-APR-1993
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 06/175,155
 ; FILING DATE: 24-DEC-1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Tiscartin, Richard F.
 ; REGISTRATION NUMBER: 31,801
 ; REFERENCE/DOCKET NUMBER: A-5150 EFFECTIVITY
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 415 791-1989
 ; TELEFAX: 415 798-3242
 ; INFORMATION FOR SEQ. NO. 20:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 285 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 US 08 492 085P 20

Query Match 55.43, Score 47, DB 3, Length 285;

Best Local Similarity 90.98, Pred. No. 12; Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 KKKKKKSPSKS 14
 : ||||| :
 Db 2 PPKKKKSPSKS 73

RESULT 5
 US-08-570-311-4
 ; Sequence 4, Application US/08570311

1 TITLE OF INVENTION: C1oned Porphyromonas gingivalis Genes
2 TITLE OF INVENTION: and Probes for the Detection of Periodontal Disease
3 NUMBER OF SEQUENCES: 29
4 CORRESPONDENCE ADDRESS:
5 ADDRESSEE: Ted W. Whitlock
6 STREET: 2421 N.W. 41st Street, Suite A-1
7 CITY: Gainesville
8 STATE: FL
9 COUNTRY: USA
10 ZIP: 32606
11 COMPUTER READABLE FORM:
12 MEDIUM TYPE: Floppy disk
13 COMPUTER: IBM PC compatible
14 OPERATING SYSTEM: PC DOS/MS-DOS
15 SOFTWARE: PatentIn Release #1.0, Version #1.0a
16 CURRENT APPLICATION DATA:
17 APPLICATION NUMBER: US 07/576,311
18 FILING DATE: 25-JAN-1991
19 CLASSIFICATION: 424
20 PRIOR APPLICATION DATA:
21 APPLICATION NUMBER: US 06/352,485
22 FILING DATE: 09-DEC-1994
23 CLASSIFICATION: 424
24 PRIOR APPLICATION DATA:
25 APPLICATION NUMBER: US 07/647,119
26 FILING DATE: 25-JAN-1991
27 CLASSIFICATION: 424
28 PRIOR APPLICATION DATA:
29 APPLICATION NUMBER: US 07/441,640
30 FILING DATE: 08-SEP-1988
31 ATTORNEY/AGENT INFORMATION:
32 NAME: Whitlock, Ted W.
33 REGISTRATION NUMBER: 36,965
34 REFERENCE/DOCKET NUMBER: UF15.03
35 TELECOMMUNICATION INFORMATION:
36 TELEPHONE: (904) 375-9160
37 TELEFAX: (904) 372-5800
38 INFORMATION FOR SEQ ID NO: 6:
39 SEQUENCE CHARACTERISTICS:
40 LENGTH: 350 amino acids
41 TYPE: amino acid
42 TOPOLOGY: linear
43 MOLECULE TYPE: protein
44 US-08-570-311-6
45
46 Query Match 53.0%; Score 44; DB: Length 350
47 Best Local Similarity 61.5%; Pred. NO: 29;
48 Matches 8; Conservative 2; Mismatches 3; Indels 0
49
50 Cy 3 PEPPEPEPEPEKSS 15
51 ||| ||||| :
52 Db 307 PPKKKKKPASST 319
53
54 RESULT 7
55 US-08-353-485-4
56 Sequence 4, Application US/08353485
57 Patent No. 5830710
58 GENERAL INFORMATION:
59 APPLICANT: Progluske-Fox, Ann
60 APPLICANT: Tumwasorn, Somying
61 APPLICANT: Lepine, Guylaine
62 APPLICANT: Han, Nairing
63 APPLICANT: Lantz, Marilyn
64 APPLICANT: Patti, Joseph
65 TITLE OF INVENTION: C1oned Porphyromonas gingivalis Genes
66 TITLE OF INVENTION: and Probes for the Detection of Periodontal Disease
67 NUMBER OF SEQUENCES: 12
68 CORRESPONDENCE ADDRESS:
69 ADDRESSEE: Ted W. Whitlock
70 STREET: 2421 N.W. 41st Street, Suite A-1
71 CITY: Gainesville
72 STATE: FL

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QY 1 DPKK--KKKKSPKSS 15
DB 291 DDPKPKKPKKPKKPKK 369

RESULT 12
US-09-072-783-1
; Sequence 1, Application US/08972783
; Patent No. 5989717
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Lal, Preeti
; TITLE OF INVENTION: HUMAN PERLIN BINDING PROTEIN
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Theye Pharmaceuticals, Inc.
; STREET: 114 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/972,783
; FILING DATE: Herewith
; CLASSIFICATION: 425
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Hillinger, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: FF 0317 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-955-0555
; TELEFAX: 415-945-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 151 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: TESTT002
; CLONE: 2345085
US-09-072-783-1

Query Match 51.8%; Score 42; DB 2; Length 151;
Best Local Similarity 80.0%; Pred. No. 18;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 KKKKSPKSS 13
DB 49 KKKKPKPKPKPKPKPK 19

RESULT 13
US-09-533-669A-18
; Sequence 18, Application US/08972783
; Patent No. 5984592
; GENERAL INFORMATION:
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: BIGHANARIA ANTIGENS FOR USE IN THE
; TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF BIGHANARIASIS
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Reed and Berry LLP
; STREET: 4300 Columbia Center, 701 Fifth Avenue

```

```

; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: Windows/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/972,783
; FILING DATE: 22-SEP-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Mark, David J.
; REGISTRATION NUMBER: 31,902
; REFERENCE/DOCKET NUMBER: 210241420
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 732 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-533-669A-18

Query Match 51.8%; Score 43; DB 4; Length 732;
Best Local Similarity 79.2%; Pred. No. 84;
Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 DDPKPKKPKKPKKPKK 13
DB 271 DDPKPKKPKKPKKPKK 283

RESULT 14
US-09-307-143-4
; Sequence 4, Application US/09007143
; Patent No. 6335157
; GENERAL INFORMATION:
; APPLICANT: Gonzalez C.
; APPLICANT: Lange, B.
; TITLE OF INVENTION: METHODS BASED ON LOCALIZATION OF HSP90 TO THE
; FILE REFERENCE: 9882-003
; CURRENT APPLICATION NUMBER: US/09/307,143
; CURRENT FILING DATE: 1999-05-07
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 732
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-307-143-4

Query Match 51.8%; Score 43; DB 4; Length 732;
Best Local Similarity 79.2%; Pred. No. 84;
Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 DDPKPKKPKKPKKPKK 13
DB 271 DDPKPKKPKKPKKPKK 283

RESULT 15
US-08-183-861-18
; Sequence 18, Application US/08972783
; Patent No. 6365165
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Corixa Corp., Antonio

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RESULT 9
PTHR_MOUSE
ID PTHR_MOUSE STANDARD, PRT: 175 AA
AC P22858;
DT 01-AUG-1991 (rel 14, last sequence update)
DT 01-AUG-1991 (rel 14, last sequence update)
DT 16-OCT-2001 (rel 40, last annotation update)
DE Parathyroid hormone related protein precursor (PTH-rp) (PTHrP) (PTHr)
GN PTHLH OR PTHRP
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91065532; PubMed 2349778;
RA Martin W., Ikeda Y., Broadus A.E.;
RT "Structure of the mouse gene encoding parathyroid hormone-related
RT peptide."
RL Gene 92136; 2021(1990).
CC ENTREZY FOLLOWS A PHYSIOLOGICAL ROLE IN LACTATION, POSSIBLY AS A
CC HORMONE FOR THE MOBILIZATION AND/OR TRANSFER OF CALCIUM TO THE
CC MILK.
CC -- SUBCELLULAR LOCATION: Secreted.
CC -- SIMILARITY: BELONGS TO THE PARATHYROID HORMONE FAMILY.
CC This SWISS-PROT entry is copyright 1991. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use, by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement. (See http://www.isb.ch/announce/
CC or send an email to license@isb-sib.ch.)
CC --
CC EMBL: M60059; AA063633.1;
CC EMBL: M60059; AA063633.1; JOINED.
CC EVR1: 42556; AA063633.1; JOINED.
CC PIR: JN0103; JN0103.
CC DR HSPD; P12372; 1B23.
CC DR MGD; MGI:97809; Pthlh.
CC InterPro: IPR003626; PTH related.
CC Pfam: PF01270; Parathyroid_hrm.
CC ProDom: PD013225; PTH related; 1.
CC SMART; SM0087; PTH; 1.
CC PROSITE; PS00335; PARATHYROID; 1.
CC KX Calcium; Hormone; Signal.
CC FT SIGNAL 1 24 POTENTIAL.
CC FT PROPEP 25 34
CC FT CHAIN 37 175 PARATHYROID HORMONE-RELATED PROTEIN.
CC S: REFERENCE 175 AA, 36,000 MW, 652/250019, 4045 JB64,
Query Match 59.6%, Score 42, PP 1, Length 177,
Best Local Similarity 75.0%, Pred No. 1.87,
Matches 9, Conservations 1, Mismatches 2, Indels 0, Gaps 6;
QY 4 KPSKSKKKKPG 15
Dh 120 VTPGVYVYVPG 131
|:|:|:|:|:|:|
RESULT 10
PTHR_CANFA
ID PTHR_CANFA STANDARD, PRT: 177 AA.
AC P52211;
DT 01-OCT-1994 (rel 34, last sequence update)
DT 01-OCT-1994 (rel 34, last sequence update)
DT 16-OCT-2001 (rel 40, last annotation update)
DE Parathyroid hormone-related protein precursor (PTH-rp) (PTHrP)
GN PTHLH.
OS Canis familiaris (Dog)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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Ob 120 KPSKYYKYPG 131

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RESULT 12
PTHR RABIT

ID PTHR RABIT STANDARD; PRT; 177 AA.
AC Q2GLC1;
DT 16-OCT-2001 (rel. 40, Created)
DT 16-OCT-2001 (rel. 40, Last sequence update)
DT 16-OCT-2001 (rel. 40, Last annotation update)
DE Parathyroid hormone-related protein precursor (PTHrP) (PTHRP)
GN PTHRHR OR PTHRP.
CC "This is a highly conserved protein."
CC Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
CC Mammalia, Eutheria, Lagomorpha, Leporidae, Cytodactylus.
CA NCBI TaxID 9986.
(1) _TaxID 9986.
RN SEQUENCE FROM N.A.
RP McCaughern-Carpel J.E., Winkler M., Emanuel J.P., Iwerczyk S.J.;
RA "Cloning and expression of rabbit parathyroid hormone-related
RT protein."
RL Sub-1 and "Antigen" - the EMBL/Genbank/CCDS databases
CC -1- FUNCTION: PLAYS A PHYSIOLOGICAL ROLE IN LACTATION, POSSIBLY AS A
CC HORMONE FOR THE MOBILIZATION AND/OR TRANSFER OF CALCIUM TO THE
CC MILK.
CC -2- SUBCELLULAR LOCATION: Secreted.
CC -3- SIMILARITY: BELONGS TO THE PARATHYROID HORMONE FAMILY.
CC This SWISS-PROT entry is copyrighted. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC at the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
CC or send an email to license@sib-sib.ch).
CC EMBL; AF300703; MAG13414.1; -
CC HCSF; F22272; IBCG.
CC InterPro; IPR001415; Parathyroid_hrm.
CC Pfam; PF01379; Parathyroid; 1.
CC ProDom; PD013225; PTH related; 1.
CC SMART; SM00387; PTH, 1.
CC ProSite; PS00435; PAPATHYROID; 1.
CC Calcium; Hormone; Signal.
FT SIGNAL; 1 34 POTENTIAL.
FT PROPEP; 25 34 BY SIMILARITY.
FT CHAIN; 37 177 PARATHYROID HORMONE-RELATED PROTEIN.
CC SEQUENCE 177 AA; 20005 MW; ELD9F427657E19 QR264;
Query Match 59.0%; Score 49; DP 1; Length 177;
Best Local Similarity 76.0%; Pred. No 18;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 KPSKYYKYPG 15
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DB 120 KPSKYYKYPG 131

RESULT 13

ID PTHR RAT STANDARD; PRT; 177 AA.
AC P13085;
DT 01-JAN-1990 (rel. 13, Created)
DT 01-JAN-1990 (rel. 13, Last sequence update)
DT 16-OCT-2001 (rel. 40, Last annotation update)
DE Parathyroid hormone-related protein precursor (PTHrP) (PTHRP) (PTHR)
GN PTHRHR OR PTHRP.
CC "Parathyroid hormone-related protein (PTHrP) is a highly conserved protein."
CC Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
CC Mammalia, Eutheria, Eulipotyphla, Sciuromorpha, Muridae, Murinae, Rattus

OX NCBI_TaxID-10116;

RN SEQUENCE FROM N.A.
RX MEDLINE:99019361; PubMed:2175553;
PA Thiede M.A., Podan G.A.;
RT "Expression of a calcium mobilizing parathyroid hormone like peptide
RT in lactating mammary tissue."
SL Science 242:278-280(1988).
RN SEQUENCE FROM N.A.
RP MEDLINE:99019361; PubMed:2175553;
PA Yasuda T., Parvillo D., Pabiani S.A., Hendy G.N., Goltzman D.;
RT "Parathyroid hormone-like peptide: comparison with the human
RT homologue and expression in malignant and normal tissue."
SL Endocrinol. 135:94-95(1994).

RN SEQUENCE FROM N.A.
RP MEDLINE:99019361; PubMed:2175553;
PA Yasuda T., Yasuda T., Hendy G.N., Goltzman D.;
RT "Parathyroid hormone-like peptide: comparison with the human
RT homologue and expression in malignant and normal tissue."
SL Endocrinol. 135:94-95(1994).
RN SEQUENCE FROM N.A.
RP MEDLINE:99019361; PubMed:2175553;
PA Yasuda T., Yasuda T., Hendy G.N., Goltzman D.;
RT "Parathyroid hormone-like peptide: comparison with the human
RT homologue and expression in malignant and normal tissue."
SL Endocrinol. 135:94-95(1994).

RN SEQUENCE FROM N.A.
RP MEDLINE:99019361; PubMed:2175553;
PA Yasuda T., Yasuda T., Hendy G.N., Goltzman D.;
RT "Parathyroid hormone-like peptide: comparison with the human
RT homologue and expression in malignant and normal tissue."
SL Endocrinol. 135:94-95(1994).
RN SEQUENCE FROM N.A.
RP MEDLINE:99019361; PubMed:2175553;
PA Yasuda T., Yasuda T., Hendy G.N., Goltzman D.;
RT "Parathyroid hormone-like peptide: comparison with the human
RT homologue and expression in malignant and normal tissue."
SL Endocrinol. 135:94-95(1994).

RN SEQUENCE FROM N.A.
RP MEDLINE:99019361; PubMed:2175553;
PA Yasuda T., Yasuda T., Hendy G.N., Goltzman D.;
RT "Parathyroid hormone-like peptide: comparison with the human
RT homologue and expression in malignant and normal tissue."
SL Endocrinol. 135:94-95(1994).
RN SEQUENCE FROM N.A.
RP MEDLINE:99019361; PubMed:2175553;
PA Yasuda T., Yasuda T., Hendy G.N., Goltzman D.;
RT "Parathyroid hormone-like peptide: comparison with the human
RT homologue and expression in malignant and normal tissue."
SL Endocrinol. 135:94-95(1994).

RN SEQUENCE FROM N.A.
RP MEDLINE:99019361; PubMed:2175553;
PA Yasuda T., Yasuda T., Hendy G.N., Goltzman D.;
RT "Parathyroid hormone-like peptide: comparison with the human
RT homologue and expression in malignant and normal tissue."
SL Endocrinol. 135:94-95(1994).

Query Match 59.0%; Score 49; DP 1; Length 177;
Best Local Similarity 76.0%; Pred. No 18;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 KPSKYYKYPG 15
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DB 120 KPSKYYKYPG 131

RESULT 14

ID ADDG RAT STANDARD; PRT; 205 AA.
AC Q62847;
DT 16-OCT-2001 (rel. 40, Created)
DT 16-OCT-2001 (rel. 40, Last sequence update)
DT 16-OCT-2001 (rel. 40, Last annotation update)

KW Cytoskeleton, Membrane, Calmodulin-binding, Phosphorylation;
 KW Alternative splicing.
 PT DCMAIN 584 701 CALMODULIN-BINDING (POTENTIAL).
 PT MCLRES 683 683 PHOSPHORYLATION (BY PKC) (BY SIMILARITY).
 PT VARSPLIC 576 607 MISSING (IN ISOFORM 1).
 PT CONFLICT 49 50 EN -> SS (IN REF. 1).
 PT CONFLICT 50 50 Q -> R (IN REF. 1).
 PT CONFLICT 362 362 Q -> P (IN REF. 2).
 PT CONFLICT 470 470 V -> W (IN REF. 2).
 PT CONFLICT 421 421 E -> L (IN REF. 1).
 PT CONFLICT 424 433 KIMAPRCQ -> CHISTEGRK (IN REF. 2).
 PT CONFLICT 484 484 K -> Q (IN REF. 2).
 SQ SEQUENCE 706 AA; 79134 MW; EB86AF502A4E/541 CRC64;
 Query Match 59.0%; Score 43; DB 1; Length 706;
 Best Local Similarity 100.0%; Pos. No. 7;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 3 SKSPSKKKK 12
 Db 67a SKSPSKKKK 698
 Search completed: March 3, 2003, 06:36:19
 Job time : 7.65854 secs


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RESULT 4
Q9DEU4 Q9DEU4
ID Q9DEU4 PPT: 896 AA.
AC Q9DEU4; 2001 (TrEMBLrel. 16, Created)
DT 01 MAR 2001 (TrEMBLrel. 16, Last sequence update)
DT 01 MAR 2001 (TrEMBLrel. 16, Last annotation update)
DE CCAAT box transcription factor p122 subunit.
FE CCAAT box transcription factor p122 subunit.
GC CCAAT box transcription factor p122 subunit.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenocephalae; Xenopus
CC NCBI_TaxID=8355,
OX NCBI_TaxID=8355,
RN [1]
RP SEQUENCE FROM N.A. PubMed 10890122.
RX MEDLINE: 735467, PubMed 10890122.
FA Blaszkowski J., Potkin C., Orford R., Edgar S., Scarlett G.,
FA Petrekaitis T., Maltbie W., Khale G., Warrington M., Guille M.;
FA "RNA-3 dependent cytoplasmic anchoring of a transcription factor subunit
FA during Xenopus development.";
FA EMBO J 19:3683-3693(2000).
FA SHEL, AY099240, AAC20450.1, -
FA LOC:275, 11596159, DS_PPR.
FA EF37, EF060355, termi_2
FA SMART, SM00359, DSBM_2.
FA PROSITE, PROSITE, PS_FPR_2
FE SEQUENCE 896 AA. 896aa MW: 98664407.7kDa;
Query Match 61.4%; Score 51; DB 13; Length 896;
8-est 1st similarity 81.3%; Pred No. 6.9; 2; Indeis 0; Gaps 0;
Matches 10, Conservative 0; Mismatches 2;

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DE      373 GDNFSGVPTTYY 290

RESULT 5
Q8TDIO PRELIMINARY; PRT: 1954 AA.
AC Q8TDIO;
DT 01-JUN-2000 (TEMPBLAST) C1. Created
LT 01-JUN-2000 (TEMPBLAST) C1. Last sequence update)
BT 01-JUN-2000 (TEMPBLAST) C1. Last annotation update)
DE Chromodomain helicase DNA binding protein 5.
GN CHD5.
OC Homo sapiens (Human).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
GX NCBI_Taxid=9606;
LN [1]
PP SEQUENCE FROM N.A.
RA Thompson P.M., Smith T., White P.G., Brodeur G.M.;
RT "CHD5, a New Member of the Chromodomain Gene Family, is Preferentially
   Expressed in the Nervous System";
RL Submitted (Sep 2001) to the EMBL/GenBank/DBJ databases.
DR EMBL, AF455231. AAI04927.1; -.
KW Helicase.
SQ SEQUENCE 1951 AA, 223048 MW; E333062B5B55E1F CHK54;
Query Match          61 48, Score 51; DR 4; Length 1954;
Best Local Similarity 49 48; Pval No. 14;
Matches 11; Conservative 1; Wismatches 4; Indels 0; Gaps 0;

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RESULT 6
Q962J9
ID Q962J5
PRELIMINARY,
PPT: 1025 AA


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L Submitted (MAR-2006) to the EMBL/GenBank/DBJ databases.
N [4]
P SEQUENCE FROM N.A.
L EU Arabidopsis sequencing project.
L Submitted (MAR-2006) to the EMBL/GenBank/DBJ databases.
L EMBL; AL079350; CAB4512.1; -
L EMBL; AL161563; CAB81345.1; -
R HSP; Gene44; LPEK
R InterPro: IPR001179; FKBP_PPIase
R Pfam: PF00454; FKBP; 1.
R PROSITE: PS00454; FKBP_PPIASE_2; 1.
R PROSITE: PS0059; FKBP_PPIASE_3; 1.
W Hypothetical protein
W HYPROTEIN
W SEQUENCE 487 AA, 53232 VW, 5836ACTGTCGACG GCGA,
Judy Math 50.23, Score 50, DP 10, Length 497;
Best Local Similarity 52.23; PId: No. 5.7;
Matches 10, Conservative 1, Mismatches 0, Indels 9, Gaps 1.
Y 2 SSKSPK-----PFFKPGD 16
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D 120 SSKTTPYSAEYTKNFFKYPGQ 150
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RESULT 10
Q224X4 PRELIMINARY; PRT; 175 AA
Q224X4
D Q224X4
C Q224X4;
T 01-DEC-2001 (TrEMBLrel. 19, Created)
T 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
T 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
D 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
E Parathyroid hormone-related protein precursor.
P ThrLH.
M Mus musculus (Mouse).
S Eukaryota, Metazoa, Chordata, Mammalia, Eutelestia, Eutelestia,
C Mammalia, Eutelestia, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
X NP1_TaxID=10090;
Y [1]
SEQUENCE FROM N.A.
STRAIN=C3H/HEJ; TISSUE=LUNG;
A Manenti G., Pelless B., Cariboidi M., Falvella F.S., Zaffaroni P.,
C Covelli V., Sarau A., Diagani T.A.,
T "A cancer modifier role for parathyroid hormone related protein.";
L Submitted (MAY-2006) to the EMBL/GenBank/DBJ databases.
L EMBL; AC278112; CAC19218.1.
R InterPro: IPR001415; Parathyroid hrm.
R InterPro: IPR001626; PTH related.
R Pfam: PF01279; Parathyroid, 1.
R PROSITE: PS01325; PTH related, 1.
R PROSITE: PS0045; PARATHYROID, INTERM.
W Signal.
W SIGNAL 1 36 POTENTIAL
PFT CHAIN 37 175 PARATHYROID HORMONE-RELATED PROTEIN.
S SEQUENCE 175 AA, 21046 VW, 40355CTGAGGAG GCGA,
Judy Math 59.03, Score 49, DP 11, Length 175;
Best Local Similarity 75.63; PId: No. 3.2;
Matches 9, Conservative 1, Mismatches 2, Indels 0, Gaps 0;
Y 4 KSPKPKPKPKPKG 15
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D 120 KTPCKKPKPKPKG 131
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RESULT 11
Q26023 PRELIMINARY; PRT; 202 AA.
Q26023
AC Q26023;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
L 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
C WAP-2000 (TrEMBLrel. 20, Last annotation update)
D Parathyroid hormone-related protein.
S Oryctolagus cuniculus (Rabbit).

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      28 41 49.4 412 1 US-08-313-288B-1P
      29 41 49.4 680 1 US-08-711-432-2
      30 41 49.4 680 3 US-08-761-136-1
      31 41 49.4 1123 4 US-09-408-865-1
      32 40 48.2 25 1 US-08-240-514-5A
      33 40 48.2 25 2 US-08-612-302A-5A
      34 40 48.2 25 4 US-09-039-780A-119
      35 40 48.2 27 4 US-03-424-755-2
      36 40 48.2 28 4 US-09-424-656-1
      37 40 48.2 79 4 US-09-149-476-199
      38 40 48.2 173 4 US-09-133-341-13
      39 40 48.2 329 4 US-09-651-200-1A
      40 40 48.2 576 1 US-08-190-802A-5A
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      42 40 48.2 576 4 US-08-473-089-5A
      43 40 48.2 576 4 US-08-487-072A-5A
      44 40 48.2 723 1 US-07-814-964-11
      45 40 48.2 723 1 US-08-258-442-11

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ALIGNMENTS

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RESULT 1
US-08-411-726-5
; Sequence 5, Affiliation: US-08411726
; Patent No. 5880093
; GENERAL INFORMATION:
; APPLICANT: BAGNOLI, Franco
; TITLE OF INVENTION: Use of Parathyroid, Its Biologically
; TITLE OF INVENTION: Active Fragments and Correlated Peptides, for the Preparation
; TITLE OF INVENTION: Pharmaceutical Compositions Useful for the Treatment of
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESS: Kenyon & Kenyon
; STREET: 1 Broadway
; CITY: New York
; STATE: NY
; COUNTRY: US
; ZIP: 10004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS 5.2
; SOFTWARE: WordPerfect 6.1 for Windows
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP93/02765
; FILING DATE: 29-OCT-1993
; APPLICATION NUMBER: US/89/411,726
; FILING DATE: 05-APR-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP93/02765
; FILING DATE: 29-OCT-1993
; APPLICATION NUMBER: MI 92A002331
; FILING DATE: 09-OCT-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: PALMESE, Maria Luisa
; REGISTRATION NUMBER: 34,402
; REFERENCE/KEYWORD NUMBER: C111/0300
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 422 7200
; TELEFAX: 212-425-5288
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 141 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-411-726-5

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      29 41 49.4 680 1 US-08-711-432-2
      30 41 49.4 680 3 US-08-761-136-1
      31 41 49.4 1123 4 US-09-408-865-1
      32 40 48.2 25 1 US-08-240-514-5A
      33 40 48.2 25 2 US-08-612-302A-5A
      34 40 48.2 25 4 US-09-039-780A-119
      35 40 48.2 27 4 US-03-424-755-2
      36 40 48.2 28 4 US-09-424-656-1
      37 40 48.2 79 4 US-09-149-476-199
      38 40 48.2 173 4 US-09-133-341-13
      39 40 48.2 329 4 US-09-651-200-1A
      40 40 48.2 576 1 US-08-190-802A-5A
      41 40 48.2 576 4 US-08-477-346-5A
      42 40 48.2 576 4 US-08-473-089-5A
      43 40 48.2 576 4 US-08-487-072A-5A
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Best Local Similarity 41.0% E-12, Fred. No. 47
Matches 9, Conservative 1, Mismatched 0, Indels 0, Gaps 0

QY 4 KPSKPKKPKPKG 15
 DB 44 KPSKPKKPKPKG 95

RESULT 2

Patent No. 5217896
 APPLICANT: FRAMER, STEVEN P; VALENTELA, DAVID M; FERNANDES
 JR., FREDERICK H; SOPAVILLO, JOHN M.
 TITLE OF INVENTION: MONOCLONAL ANTIBODIES FOR TREATING
 PARATHYROID HORMONE-LIKE PROTEIN
 NUMBER OF SEQUENCES: 8
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/07/292,263
 FILING DATE: 30-DEC-1988
 SEQ ID NO: 3:
 LENGTH: 141

5217896-3

Query Match 59.0%; Score 49; DB 6; Length 141;
 Best Local Similarity 75.0%; Pred. No. 4;
 Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 KPSKPKKPKPKG 15
 DB 44 KPSKPKKPKPKG 95

RESULT 3

US-09-643-597-165
 Sequence 165, Application US/09643597
 Patent No. 6426072
 GENERAL INFORMATION:

APPLICANT: Wang, Tongtong
 APPLICANT: Fan, Liqun
 APPLICANT: Kalos, Michael D.
 APPLICANT: Bangur, Chaitanya S.
 APPLICANT: Hosken, Nancy
 APPLICANT: Fanger, Gary R.
 APPLICANT: Li, Samuel X.
 APPLICANT: Wang, Aijun
 APPLICANT: Skeiky, Yasir A W
 APPLICANT: Henderson, Robert A
 APPLICANT: McNeill, Patricia D
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
 OF LUNG CANCER
 FILE REFERENCE: 21021455C11
 CURRENT APPLICATION NUMBER: US/09/643,597
 FILING DATE: 2000-08-31
 NUMBER OF SEQ ID NOS: 369
 SOFTWARE: FastSeq for Windows Version 3.0
 SEQ ID NO 165
 LENGTH: 177
 TYPE: PRT
 ORGANISM: Homo sapien

US-09-643-597-165

Query Match 59.0%; Score 49; DB 4; Length 177;
 Best Local Similarity 75.0%; Pred. No. 5;
 Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 KPSKPKKPKPKG 15
 DB 120 KPSKPKKPKPKG 131

RESULT 4

US-09-643-597-166
 Sequence 166, Application US/09643597
 Patent No. 6426072
 GENERAL INFORMATION:

APPLICANT: Wang, Tongtong
 APPLICANT: Fan, Liqun
 APPLICANT: Kalos, Michael D.
 APPLICANT: Bangur, Chaitanya S.
 APPLICANT: Hosken, Nancy
 APPLICANT: Fanger, Gary R.
 APPLICANT: Li, Samuel X.
 APPLICANT: Wang, Aijun
 APPLICANT: Skeiky, Yasir A.W.
 APPLICANT: Henderson, Robert A.
 APPLICANT: McNeill, Patricia D.
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
 OF LUNG CANCER
 FILE REFERENCE: 21021455C11
 CURRENT APPLICATION NUMBER: US/09/643,597
 FILING DATE: 2000-08-31
 NUMBER OF SEQ ID NOS: 369
 SOFTWARE: FastSeq for Windows Version 3.0
 SEQ ID NO 166
 LENGTH: 177
 TYPE: PRT
 ORGANISM: Homo sapien

US-09-643-597-166

Query Match 59.0%; Score 49; DB 4; Length 177;
 Best Local Similarity 75.0%; Pred. No. 5;
 Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 KPSKPKKPKPKG 15
 DB 120 KPSKPKKPKPKG 131

RESULT 5

US-08-064-111C-1
 Sequence 1, Application US/0806411C
 Patent No. 5688760
 GENERAL INFORMATION:

APPLICANT: Kemp, Bruce E.
 APPLICANT: Nicholson, Geoffrey C.
 APPLICANT: Martin, Thomas J.
 APPLICANT: Fenton, Anna J.
 APPLICANT: Hammonds, R. Glenn
 TITLE OF INVENTION: COMPOSITIONS AND METHODS WHICH INHIBIT
 THE GROWTH OF CANCER CELLS
 NUMBER OF SEQUENCES: 26
 FILE REFERENCE: 21021455C11
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/064,111C
 FILING DATE: 12-AUG-1993
 CLASSIFICATION: 514
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/AU/91/00580
 FILING DATE: 13-DEC-1991
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: AU P/9567
 FILING DATE: 19-NOV-1991
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: AU P/93873
 FILING DATE: 13-DEC-1990
 ATTORNEY/AGENT INFORMATION:



Job time : 19.3415 secs

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seq 50; DB 17;
Mismatches 7; Indels 0; Gaps 1;

seq 51; DB 17;
Mismatches 7; Indels 0; Gaps 1;

seq 52; DB 17;
Mismatches 7; Indels 0; Gaps 1;

seq 53; DB 17;
Mismatches 7; Indels 0; Gaps 1;

seq 54; DB 17;
Mismatches 7; Indels 0; Gaps 1;

seq 55; DB 2; Length 144;
seq 56; DB 14;
Mismatches 5; Indels 0; Gaps 0;

seq 57; DB 2; Length 144;
seq 58; DB 14;
Mismatches 5; Indels 0; Gaps 0;

seq 59; DB 2; Length 144;
seq 60; DB 14;
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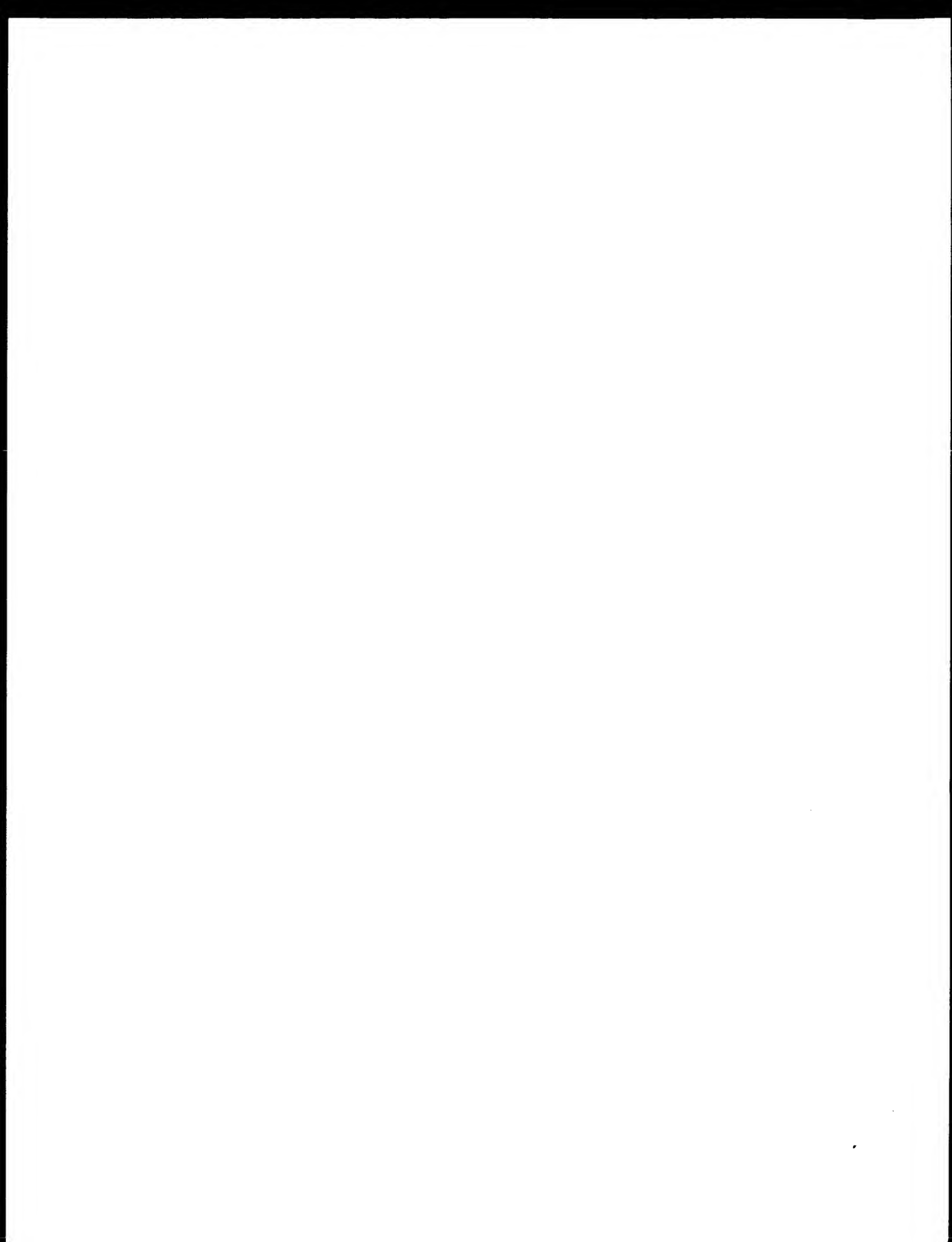
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seq 63; DB 2; Length 144;
seq 64; DB 14;
Mismatches 5; Indels 0; Gaps 0;

seq 65; DB 2; Length 144;
seq 66; DB 14;
Mismatches 5; Indels 0; Gaps 0;

seq 67; DB 2; Length 144;
seq 68; DB 14;
Mismatches 5; Indels 0; Gaps 0;

seq 69; DB 2; Length 144;
seq 70; DB 14;
Mismatches 5; Indels 0; Gaps 0;



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Best Local Similarity 55.6%; Pred. No. 9.2;
Matches 10; Conservative 3; Mismatches 5; Indels 0;
Gaps 0;

Query Match 46.2%; Score 48; DB 1; Length 497;
Best Local Similarity 55.6%; Pred. No. 9.2;
Matches 10; Conservative 3; Mismatches 5; Indels 0;
Gaps 0;

Query Match 46.2%; Score 48; DB 1; Length 497;
Best Local Similarity 55.6%; Pred. No. 9.2;
Matches 10; Conservative 3; Mismatches 5; Indels 0;
Gaps 0;

Query Match 46.2%; Score 48; DB 1; Length 497;
Best Local Similarity 55.6%; Pred. No. 9.2;
Matches 10; Conservative 3; Mismatches 5; Indels 0;
Gaps 0;

Query Match 46.2%; Score 48; DB 1; Length 497;
Best Local Similarity 55.6%; Pred. No. 9.2;
Matches 10; Conservative 3; Mismatches 5; Indels 0;
Gaps 0;

Query Match 46.2%; Score 48; DB 1; Length 497;
Best Local Similarity 55.6%; Pred. No. 9.2;
Matches 10; Conservative 3; Mismatches 5; Indels 0;
Gaps 0;

Query Match 46.2%; Score 48; DB 1; Length 497;
Best Local Similarity 55.6%; Pred. No. 9.2;
Matches 10; Conservative 3; Mismatches 5; Indels 0;
Gaps 0;

Query Match 46.2%; Score 48; DB 1; Length 497;
Best Local Similarity 55.6%; Pred. No. 9.2;
Matches 10; Conservative 3; Mismatches 5; Indels 0;
Gaps 0;

Query Match 46.2%; Score 48; DB 1; Length 497;
Best Local Similarity 55.6%; Pred. No. 9.2;
Matches 10; Conservative 3; Mismatches 5; Indels 0;
Gaps 0;

Query Match 46.2%; Score 48; DB 1; Length 497;
Best Local Similarity 55.6%; Pred. No. 9.2;
Matches 10; Conservative 3; Mismatches 5; Indels 0;
Gaps 0;

Query Match 46.2%; Score 48; DB 1; Length 497;
Best Local Similarity 55.6%; Pred. No. 9.2;
Matches 10; Conservative 3; Mismatches 5; Indels 0;
Gaps 0;

Query Match 46.2%; Score 48; DB 1; Length 497;
Best Local Similarity 55.6%; Pred. No. 9.2;
Matches 10; Conservative 3; Mismatches 5; Indels 0;
Gaps 0;

is as long as it's not in no way
not removed. Usable for commercial
purpose. (See <http://www.sle.ch/announce/>
: sle.ch).

Postscript: I have my own
SERVATION BY EPA OF COMMUNITY
S. S. IN P.O.
FARMEREDHODDIA 1974

Core 4: DB 1: 1000.41
Vol. No. 12: 1000.41
Miscellaneous 4: 1000.41 Gaps 0:




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Nucleo  2,  Conservative  2,  Mismatches  4,  Gaps  0,
Cv  1  SPSNTHPTTPTTPTTPTT 15
    ||| ||| ||| |||
Dd  38  SPEGETPKAPPPPLS 52

RESULT 5
Q8VH64      SEQUENCE FROM N.A.
ID  Q8VH64      PRELIMINARY:      PPT:      60 AA.
AC  Q8VH64;
DT  01-MAR-2003 (TRENDEL 20, Created)
DT  01-MAR-2003 (TRENDEL 20, Last sequence update)
DT  01-MAR-2003 (TRENDEL 20, Last annotation update)
DE  01-MAR-2003 (TRENDEL 20, Last annotation update)
DE  01-MAR-2003 (TRENDEL 20, Last annotation update)
DE  01-MAR-2003 (TRENDEL 20, Last annotation update)
GN  Zf3a
CS  Mus musculus (Shrew mouse)
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus
OX  NCBI_TaxID=10091
RN  [1]
RP  SEQUENCE FROM N.A.
FA  Lendingin B, Jansa S.A., Tucker P.K.,
RT  "Phylogenetic relationships in the genus Mus, based on maternally,
RT  paternally, and biparentally inherited characters.",
RL  Syst. Biol. 50:6-8(2001).
DP  PMR1; AY057266; AAL23805 1;
FT  NON-TER
FT  NON-TER
S.  SEQUENCE 60 AA, 45% MW, 10697ELP3A23443 QP244,

Query Match 47.1%, Score 40, PP 12, Length 72,
Best Local Similarity 47.1%, Pred No. 3.1,
Matches 2, Conservative 4, Mismatches 6, Indels 0, Gaps 0,
Cv  1  SPSNTHPTTPTTPTTPTT 15
    ||| ||| ||| |||
Dd  1  AFANATCTCTACACENKT 19

RESULT 10
Q8VH73      SEQUENCE FROM N.A.
ID  Q8VH73      PRELIMINARY:      PPT:      72 AA.
AC  Q8VH73;
DT  01-MAR-2003 (TRENDEL 20, Created)
DT  01-MAR-2003 (TRENDEL 20, Last sequence update)
DT  01-MAR-2003 (TRENDEL 20, Last annotation update)
DE  01-MAR-2003 (TRENDEL 20, Last annotation update)
DE  01-MAR-2003 (TRENDEL 20, Last annotation update)
DE  01-MAR-2003 (TRENDEL 20, Last annotation update)
GN  Wsv114 (WSSV170).
CS  White spot syndrome virus (WSSV).
OC  Viruses; unclassified viruses.
OX  NCBI_TaxID=22522,
RN  [1]
RP  SEQUENCE FROM N.A.
FA  MEDLINE:2254811, PubMed:11690662,
RT  Yang F., He J., Lin X., Li Q., Fan D., Zhang X., Xu X.,
RT  "Complete genome sequence of the shrimp white spot bacilliform
RT  virus.",
RL  J. Virol. 75:11811-11820(2001).
RN  [2]
RP  SEQUENCE FROM N.A.
FA  Yang F., He J., Lin X., Li Q., Fan D., Zhang X., Xu X.,
RT  Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
RN  [3]
RP  SEQUENCE FROM N.A.
ID  Q8VH74      PRELIMINARY:      PPT:      313 AA.
AC  Q8VH74;
DT  01-MAY-2000 (TRENDEL 13, Created)
DT  01-MAY-2000 (TRENDEL 13, Last sequence update)
DT  01-MAY-2000 (TRENDEL 13, Last annotation update)
DE  01-MAY-2000 (TRENDEL 13, Last annotation update)
DE  01-MAY-2000 (TRENDEL 13, Last annotation update)
DE  01-MAY-2000 (TRENDEL 13, Last annotation update)
GN  Tip17 (Tip of A403000).
CS  Arabidopsis thaliana (Mouse-ear cress).
OC  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC  Spermatophyta; Magnoliopsida; Malvales; Malvaceae; Rosidae;

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PT  SEQUENCE FROM N.A.
RC  STRAIN=TAIWAN;
PX  MEDLINE:21844071, PubMed:11653198;
PA  Chen L.L., Liu J.H., Huang C.J., Chou C.M., Chen S.M., Wang C.H.,
RA  Lo C.F., Kou G.H.;
RT  "Identification of a nucleocapsid protein (NP1) gene of shrimp white
RT  spot syndrome virus and characterization of the motif important for
RT  targeting VP35 to the nuclei of transfected insect cells";
PL  Virology 293:44-53(2002).
RN  [5]
RP  SEQUENCE FROM N.A.
FA  Lo C.F., Kou G.H.;
RT  Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
PL  SUBMITTED (DEC-2001) to the EMBL/GenBank/DBJ databases.
DP  EMBL; AF332623; AAL33118 1;
DP  EMBL; AF440670; AAL80038 1;
S.  SEQUENCE 72 AA, 45% MW, 10697ELP3A23443 QP244,

Query Match 47.1%, Score 40, PP 12, Length 72,
Best Local Similarity 47.1%, Pred No. 3.1,
Matches 10, Conservative 3, Mismatches 4, Indels 0, Gaps 0,
Cv  2  PSNTHPTTPTTPTTPTT 18
    ||| ||| ||| |||
Dd  52  PSNTHPTTPTTPTTPTT 69

RESULT 11
Q9IAJ5      PRELIMINARY:      PPT:      197 AA.
AC  Q9IAJ5;
DT  01-OCT-2000 (TRENDEL 15, Created)
DT  01-OCT-2000 (TRENDEL 15, Last sequence update)
DT  01-OCT-2000 (TRENDEL 15, Last annotation update)
DE  01-OCT-2000 (TRENDEL 15, Last annotation update)
DE  01-OCT-2000 (TRENDEL 15, Last annotation update)
DE  01-OCT-2000 (TRENDEL 15, Last annotation update)
GN  MARCKS-related-protein-like protein.
CS  Xenopus laevis (African clawed frog).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Amphibia; Anura; Vertebrata; Pipidae; Pipidae;
OC  Xenopodinae; Xenopus.
OX  NCBI_TaxID=8355,
RN  [1]
RP  SEQUENCE FROM N.A.
FA  Zhao H., Cao H., Grunz H.;
RT  "Xenopus laevis (African clawed frog)
RT  library.",
PL  Submitted (SEP 1999) to the EMBL/GenBank/DBJ databases.
DP  EMBL; AF187864; AAF13362 1;
DP  InterPro, IP000101, MAPKs.
DP  PRINTS; P00003; MAPKs.
S.  SEQUENCE 197 AA, 107% MW, 10697ELP3A23443 QP244,

Query Match 47.1%, Score 40, PP 12, Length 187,
Best Local Similarity 47.1%, Pred No. 8.8,
Matches 12, Conservative 1, Mismatches 3, Indels 8, Gaps 1,
Cv  2  PSNTHPTTPTTPTTPTT 17
    ||| ||| ||| |||
Dd  62  PSNTHPTTPTTPTTPTT 85

RESULT 12
Q9SU24      PRELIMINARY:      PPT:      313 AA.
AC  Q9SU24;
DT  01-MAY-2000 (TRENDEL 13, Created)
DT  01-MAY-2000 (TRENDEL 13, Last sequence update)
DT  01-MAY-2000 (TRENDEL 13, Last annotation update)
DE  01-MAY-2000 (TRENDEL 13, Last annotation update)
DE  01-MAY-2000 (TRENDEL 13, Last annotation update)
DE  01-MAY-2000 (TRENDEL 13, Last annotation update)
GN  Tip17 (Tip of A403000).
CS  Arabidopsis thaliana (Mouse-ear cress).
OC  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC  Spermatophyta; Magnoliopsida; Malvales; Malvaceae; Rosidae;

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QY 1 SPSNETPPPPPPPPPP 18
DT 00 0000000000000000 45

Search completed: March 3, 2003, 06:14:49
Job time : 46.4146 secs

12.832 Millibits/Sec

12.832

12.832 / Search type: Randoms
(without alignment)

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20 43 41.3 363 9 US-09-738-626-337

21 43 41.3 396 9 US-09-764-868-811

22 43 41.3 496 10 US-09-784-289-2

23 43 41.3 1036 12 US-10-034-862-2

24 42 40.4 195 10 US-09-764-864-854

25 41 39.4 52 10 US-09-764-877-1553

26 41 39.4 53 10 US-09-864-761-42868

27 41 39.4 170 9 US-09-984-245-188

28 41 39.4 232 9 US-10-164-801-4

29 41 39.4 232 10 US-09-738-626-337

30 41 39.4 265 10 US-09-815-442-1688

31 41 39.4 397 9 US-10-044-442-17

32 41 39.4 537 9 US-09-891-139A-12

33 40 38.9 255 10 US-09-764-864-854

34 40 38.5 63 10 US-09-764-864-854

35 40 38.5 71 10 US-09-864-761-44753

36 40 38.5 71 10 US-09-864-761-44753

37 40 38.5 71 10 US-09-784-869-1169

38 40 38.5 76 10 US-09-764-869-960

39 40 38.5 76 10 US-09-764-869-960

40 40 38.5 84 12 US-10-001-843-190

41 40 38.5 116 10 US-09-764-863-738

42 40 38.5 266 10 US-09-864-761-44753

43 40 38.5 369 10 US-09-925-300-10

44 40 38.5 494 10 US-09-764-864-854

45 40 38.5 704 9 US-10-170-656-2

ALIGNMENTS

RESULT 1
US-09-925-300-517
US-09-925-300-517, Alignment: 100%
Patent No. US2000044941A1
GENERAL INFORMATION:
APPLICANT: Rosen et al
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA104
CURRENT APPLICATION NUMBER: US/09/925,302
CURRENT FILING DATE: 2001-08-10
PRIORITY APPLICATION NUMBER: PCT/US00/05918
PRIORITY FILING DATE: 2000-03-08
PRIORITY APPLICATION NUMBER: 00/124,470
PRIORITY FILING DATE: 1998-03-12
NUMBER OF SEQ ID NOS: 896
SOFTWARE: Patent in Ver. 2.0
SEQ ID NO 517
LENGTH: 247
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (1)
OTHER INFORMATION: Xaa equals any of the naturally occurring L amino acids
NAME/KEY: SITE
LOCATION: (6)
OTHER INFORMATION: Xaa equals any of the naturally occurring L amino acids
NAME/KEY: SITE
LOCATION: (23)
OTHER INFORMATION: Xaa equals any of the naturally occurring L amino acids
NAME/KEY: SITE
LOCATION: (81)
OTHER INFORMATION: Xaa equals any of the naturally occurring L amino acids
US 09 925-302-517

Query Match 61.18; Score 83.57; E-10; Length 148
Best Local Similarity 82.48; Pred. No. 0.15;
Matches 14; Conservative 0; Mismatches 2; Indels 1; Gaps 13

CY 2 PNEYTKYKYPSPK 13

DB 133 PKETPKPKPKPKPK 148

Results predicted by chance to have a
the score of the results being printed,
the total score is 13.131313.

SWAPLES

Description

Sequence 517, App
Sequence 42, Appl
Sequence 26, Appl
Sequence 43, Appl
Sequence 27, Appl
Sequence 8, Appl
Sequence 7, Appl
Sequence 12, Appl
Sequence 21, Appl
Sequence 15, Appl
Sequence 9, Appl
Sequence 6, Appl
Sequence 10, Appl
Sequence 7, Appl
Sequence 2, Appl
Sequence 2672, A
Sequence 1087, Ap
Sequence 649, App

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RESULT 4
US-09-999-745-42
? Sequence 42, Application US/0999745
? Patent No. US2002015720A1
? GENERAL INFORMATION:
? APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
? APPLICANT: Tsien, Roger Y.
? APPLICANT: Baird, Geoffrey
? TITLE OF INVENTION: CIRCULARLY PERMUTED FLUORESCENT PROTEIN INDICATORS
? FILE REFERENCE: REGEN1470-1
? CURRENT APPLICATION NUMBER: US/0999745
? PRIOR FILING DATE: 1999-05-21
? PRIOR FILING DATE: 1999-05-21
? NUMBER OF SEQ ID NOS: 21
? SOFTWARE: Patent in version 3.0
? SEQ ID NO 42
? LENGTH: 25
? TYPE: PRT
? ORGANISM: Rattus norvegicus
US-09-999-745-42

Query Match: 57.9%, Score: 60, DB: 9, Length: 25,
Best Local Similarity: 100%, Field No: 1, 0;
Matches: 12; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

QY 9 KKKKPPSPFF 19
| | | | |
DB 1 KKKKPPSPFF 12

RESULT 5
US-09-554-000-27
? Sequence 27, Application US/09554000
? Patent No. US2002015720A1
? GENERAL INFORMATION:
? APPLICANT: Tsien, Roger Y.
? APPLICANT: Miyawaki, Atsushi
? TITLE OF INVENTION: FLUORESCENT PROTEIN SENSORS FOR
? TITLE OF INVENTION: DETECTION OF ANALYTES
? FILE REFERENCE: 02352/042001
? CURRENT APPLICATION NUMBER: US/09554000
? PRIOR FILING DATE: 2000-04-20
? PRIOR APPLICATION NUMBER: 09/041,050
? PRIOR FILING DATE: 1997-03-14
? NUMBER OF SEQ ID NOS: 56
? SOFTWARE: FastSeq for Windows Version 4.0
? SEQ ID NO 27
? LENGTH: 24
? TYPE: PRT
? ORGANISM: Mus musculus
US-09-554-000-27

Query Match: 47.3%, Score: 42, DB: 9, Length: 24,
Best Local Similarity: 100%, Field No: 1, 0;
Matches: 9; Conservative: 1; Mismatches: 0; Indels: 0; Gaps: 0;

QY 9 KKKKPPSPFF 18
| | | | |
DB 1 KKKKPPSPFF 10

RESULT 6
US-09-884-681-8
? Sequence 8, Application US/09884681
? Patent No. US2002015720A1
? GENERAL INFORMATION:
? APPLICANT: Tsien, Roger Y.
? APPLICANT: Cubitt, Andrew B.
? TITLE OF INVENTION: Assays for Protein Kinases Using
? TITLE OF INVENTION: Fluorescent Protein Substrates
? NUMBER OF SEQUENCES: 48
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Townsend and Townsend and Crew LLP
? STREET: Two Embarcadero Center, Fifth Floor
? CITY: San Francisco
? STATE: California
? COUNTRY: USA
? ZIP: 94111-3834
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible

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? FILE REFERENCE: REGEN1470-1
? CURRENT APPLICATION NUMBER: US/0999745
? PRIOR FILING DATE: 1999-05-21
? PRIOR FILING DATE: 1999-05-21
? NUMBER OF SEQ ID NOS: 21
? SOFTWARE: Patent in version 3.0
? SEQ ID NO 43
? LENGTH: 24
? TYPE: PRT
? ORGANISM: Mus musculus
US-09-999-745-43

Query Match: 47.3%, Score: 42, DB: 9, Length: 24,
Best Local Similarity: 100%, Field No: 1, 0;
Matches: 9; Conservative: 1; Mismatches: 0; Indels: 0; Gaps: 0;

QY 9 KKKKPPSPFF 18
| | | | |
DB 1 KKKKPPSPFF 10

RESULT 5
US-09-554-000-27
? Sequence 27, Application US/09554000
? Patent No. US2002015720A1
? GENERAL INFORMATION:
? APPLICANT: Tsien, Roger Y.
? APPLICANT: Miyawaki, Atsushi
? TITLE OF INVENTION: FLUORESCENT PROTEIN SENSORS FOR
? TITLE OF INVENTION: DETECTION OF ANALYTES
? FILE REFERENCE: 02352/042001
? CURRENT APPLICATION NUMBER: US/09554000
? PRIOR FILING DATE: 2000-04-20
? PRIOR APPLICATION NUMBER: 09/041,050
? PRIOR FILING DATE: 1997-03-14
? NUMBER OF SEQ ID NOS: 56
? SOFTWARE: FastSeq for Windows Version 4.0
? SEQ ID NO 27
? LENGTH: 24
? TYPE: PRT
? ORGANISM: Mus musculus
US-09-554-000-27

Query Match: 47.3%, Score: 42, DB: 9, Length: 24,
Best Local Similarity: 100%, Field No: 1, 0;
Matches: 9; Conservative: 1; Mismatches: 0; Indels: 0; Gaps: 0;

QY 9 KKKKPPSPFF 18
| | | | |
DB 1 KKKKPPSPFF 10

RESULT 6
US-09-884-681-8
? Sequence 8, Application US/09884681
? Patent No. US2002015720A1
? GENERAL INFORMATION:
? APPLICANT: Tsien, Roger Y.
? APPLICANT: Cubitt, Andrew B.
? TITLE OF INVENTION: Assays for Protein Kinases Using
? TITLE OF INVENTION: Fluorescent Protein Substrates
? NUMBER OF SEQUENCES: 48
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Townsend and Townsend and Crew LLP
? STREET: Two Embarcadero Center, Fifth Floor
? CITY: San Francisco
? STATE: California
? COUNTRY: USA
? ZIP: 94111-3834
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible

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DOS/MS DOS
Release #1.0, Version #1.0

15/03/884,681

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DOS/MS DOS
Release #1.0, Version #1.0

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DOS/MS DOS
Release #1.0, Version #1.0

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US-10-003-671A-23
; Sequence 23, Application US/10000671A
; Patent No. US600015600A1
; GENERAL INFORMATION:
; APPLICANT: MIZE, ET AL
; TITLE OF INVENTION: NOVEL INTERLEUKIN-1 HVC MATERIALS AND METHODS
; CURRENT APPLICATION NUMBER: US/10/003,671A
; FILE REFERENCE: 08110/36859A
; PRIORITY FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: US 00/245,346
; PRIOR FILING DATE: 2000-11-02
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 23
; LENGTH: 151
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-003-671A-23

Query Match 42.3%; Score 44, DP 0, Length 151,
Best Local Similarity 52.9%; Pred. No. 34;
Matches 9, Conservative 1, Mismatches 7, Indels 0, Gaps 0,

Cy 2 PNNYKYYKYYKYYKYYK 18
Db 85 PNNYKYYKYYKYYKYYK 101

RESULT 10
US-10-095-407-15
; Sequence 15, Application US/1000407
; Patent No. US600014300A1
; GENERAL INFORMATION:
; APPLICANT: RM, YAKU
; TITLE OF INVENTION: NOVEL MOLECULES OF TANGO 77 RELATED PROTEIN FAMILY
; FILE REFERENCE: 09404/052001
; CURRENT APPLICATION NUMBER: US/10/005,407
; PRIORITY FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 00/031,850
; PRIOR FILING DATE: 2000-07-03
; PRIOR APPLICATION NUMBER: US 00/054,640
; PRIOR FILING DATE: 1997-08-04
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 15
; LENGTH: 153
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-095-407-15

Query Match 42.3%; Score 44, DP 0, Length 153,
Best Local Similarity 52.9%; Pred. No. 34;
Matches 9, Conservative 1, Mismatches 7, Indels 0, Gaps 0,

Cy 2 PNNYKYYKYYKYYKYYK 18
Db 87 PNNYKYYKYYKYYKYYK 103

RESULT 12
US-09-775-046-6
; Sequence 6, Application US/09775046
; Patent No. US600010233A1
; GENERAL INFORMATION:
; APPLICANT: Deters, Johannes Edward Maria Antonius
; APPLICANT: Timans, Jacqueline C
; APPLICANT: Pazan, J. Fernando
; APPLICANT: Kastelein, Robert A.
; TITLE OF INVENTION: MAMMALIAN TGF-BETA1, RELATED PEPTIDES AND METHODS
; FILE REFERENCE: 02010734
; CURRENT APPLICATION NUMBER: US/09/775,046
; CURRENT FILING DATE: 2001-02-01
; PRIOR APPLICATION NUMBER: 00/179,638
; PRIOR FILING DATE: 2000-02-02
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 6
; LENGTH: 153
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-775-046-6

Query Match 42.3%; Score 41, DP 10, Length 153,
Best Local Similarity 52.9%; Pred. No. 34;
Matches 9, Conservative 1, Mismatches 7, Indels 0, Gaps 0,

Cy 2 PNNYKYYKYYKYYKYYK 18
Db 97 PNNYKYYKYYKYYKYYK 103

RESULT 13
US-09-770-528-10
; Sequence 10, Application US/09770528
; Patent No. US6000164332A1
; GENERAL INFORMATION:
; APPLICANT: Hedrick, Joseph A.
; APPLICANT: Sana, Theodore P
; APPLICANT: Bazan, Fernando J.
; APPLICANT: Kastelein, Robert A.
; TITLE OF INVENTION: Mammalian Cy Kinase Related Reagents
; and Methods
```


CC Invention relates to methods of inhibiting mucus secretion by a
 CC mucus secreting cell by administering a compound that inhibits
 CC MAPKs protein-related mucus secretion. Such compounds include
 CC active fragments of MAPKs protein such as MAPK peptide (see
 CC AAY95897) and MA-PKS peptide (see AAY9587), which corresponds to a
 CC phosphorylation site of MAPKs. The inhibitory compounds can be
 CC used to treat conditions such as bronchitis, cystic fibrosis,
 CC chronic obstructive pulmonary disease, asthma, emphysema,
 CC pneumonia, influenza, rhinitis and the common cold. An alternative
 CC sequence for MAPKs is provided in AAY95899, which differs from the
 CC present sequence at 2 amino acid residues, Ala 84 (Ser) and
 CC Pro-119 (Ala).

XX Sequence 332 AA;

Query Match 94.23, Score 98, EP 01, Length 322;
 Best Local Similarity 100.0%, Prod No. 1.7e-06;
 Matches 19, Conservative 0, Mismatches 0, Indels 0, Gaps 0.

QY 1 SPSTNETPPPPPPPPPPPPPPPS 19
 ||||| ||||| ||||| ||||| |||||

DB 145 SPSTNETPPPPPPPPPPPPPPPS 163

RESULT 6

AAV95899

ID AAY95899 standard; Protein: 332 AA.

XX AAY95899;

DT 20-NOV-2000 (first entry)

DE Human myristoylated alanine rich C kinase substrate MAPKs.

FW MAPKs; myristoylated alanine-rich C kinase substrate; human;
 FW mucus secretion, inhibitory; bronchitis, asthma, cystic fibrosis,
 FW chronic obstructive pulmonary disease; pneumonia; emphysema;
 FW influenza, rhinitis, therapy.

OS Homo sapiens

XX Key Location/Qualifiers

FT Misc-difference 84 /note= "Ala in sequence of AAY95898"

FT Misc-difference 119 /note= "Pro in sequence of AAY95898"

FT Peptide 2...25 "MA-PKS peptide of AAY95897"

FT Peptide 152...176

FT /note= "MA-PKS peptide of AAY95897"

XX WQ000050002 A2.

XX 31-AUG-2000.

XX 24 FEB 2000, 2000WQ-00000000

XX 24 FEB 2000, 2000Q 0256154.

XX (UNIV OF NORTH CAROLINA STATE.

XX Li Y, Martin LD, Adler KB;

DR WPI; 2000 572036/53

DP N-PSB; AAY95899.

XX Regulating mucus secretion by a mucus-secreting cell, useful for
 FT treating e.g. bronchitis, asthma or pneumonia, by administering a
 FT compound that inhibits or enhances myristoylated alanine rich C kinase
 FT substrate protein.

XX Disclosure; Page 46-47; 56pp; English.

XX

CC The present sequence is that of human myristoylated alanine rich C
 CC kinase substrate MAPKs protein, a major cellular substrate. The
 CC invention relates to methods of inhibiting mucus secretion by a
 CC mucus secreting cell by administering a compound that inhibits
 CC MAPKs protein-related mucus secretion. Such compounds include
 CC active fragments of MAPKs protein such as MAPK peptide (see
 CC AAY95897) and MA-PKS peptide (see AAY95897), which corresponds to a
 CC phosphorylation site of MAPKs. The inhibitory compounds can be
 CC used to treat conditions such as bronchitis, cystic fibrosis,
 CC chronic obstructive pulmonary disease, asthma, emphysema,
 CC pneumonia, influenza, rhinitis and the common cold. An alternative
 CC sequence for MAPKs is provided in AAY95899, which differs from the
 CC present sequence at 2 amino acid residues, Ser-84 (Ala) and
 CC Ala-119 (Pro).

XX Sequence 332 AA;

Query Match 94.23, Score 98, EP 01, Length 332;
 Best Local Similarity 100.0%, Prod No. 1.7e-06;
 Matches 19, Conservative 0, Mismatches 0, Indels 0, Gaps 0.

QY 1 SPSTNETPPPPPPPPPPPPPPPS 19
 ||||| ||||| ||||| ||||| |||||

DB 145 SPSTNETPPPPPPPPPPPPPPPS 163

RESULT 7

AAV95898

ID AAY95898 standard; Protein: 330 AA

XX AAY95898;

DT 23-OCT-1990 (first entry)

DE High density lipoprotein (HDL) binding protein.

FW High density lipoprotein; HDL binding protein; atherosclerosis;
 FW hypercholesterolaemia; ds.

OS Homo sapiens

XX WQ00005744-A.

XX 31-MAY-1990.

XX 17-NOV-1989; 80WQ-00005169.

XX 18 NOV 1989, 88WQ 0273388.

XX (UNIV OF WASHINGTON.

XX (ZYMOGENETICS INC.

XX Oram JF, McKnight GL, Hart CE, Curtis DA;

XX WPI; 1990-193405/25.

XX N-PSB; AAY95898.

XX New mammalian proteins binding high density lipoprotein sub-class 3
 FT DNA encoding them and derived antibodies, for screening
 FT potentially therapeutic HDL analogues and for diagnosing risk of
 FT atherosclerosis.

XX Claim 4; Fig 1A-D; 79pp; English.

XX The protein product may be used to raise Abs, and the cDNA to
 CC create probes, both useful in screening for HDL analogues,
 CC agonists and antagonists, and in identifying abnormalities in the
 CC HDL binding/secretion pathway. HDL analogues can be used in treating
 CC hypercholesterolaemia and atherosclerosis.

XX Sequence 330 AA;

Query Match 62.5%; Score 65; DB 11; Length 330;

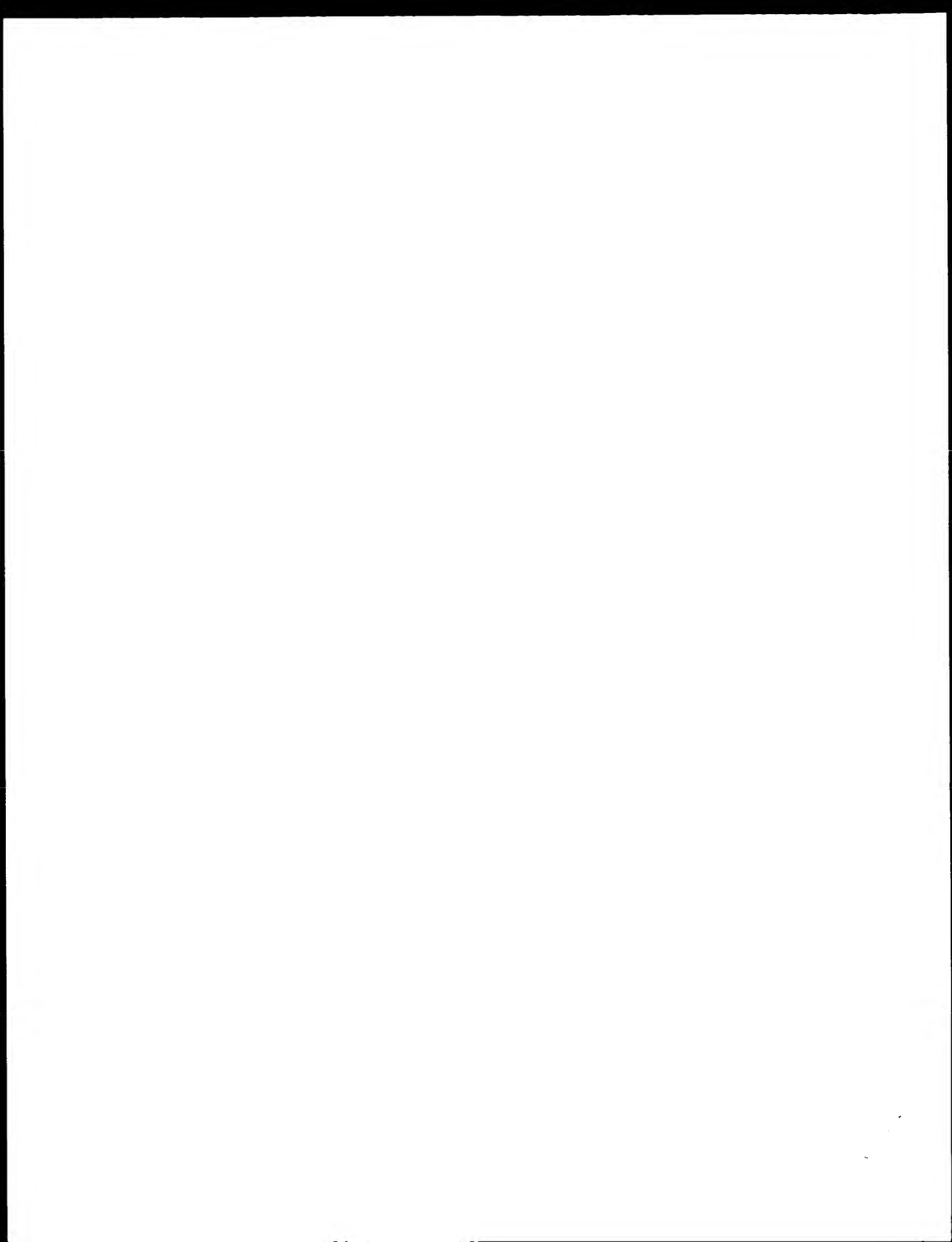
CC	therapy or cytoprotectants, diagnosing excessive apoptosis in cases of e.g. AIDS or leukodystrophy) and monitoring graft survival after transplant, as targeting agents to deliver drugs to tissues affected by loss of CMLA, and in basic research into the loss of cGMP, in vivo or in vitro. AAY51910-Y51912 represent the peptides Nst300, Nst301 and Nst302 which are described in the method of the invention.
CC	
XX	Sequence 28 AA;
SQ	
XX	Query Match 57.7%; Score 60; Pos 21; Length 28;
XX	Best Local Similarity 100.0%; Pref No 0.05;
XX	Motifs 12; Conservation 0; Mismatches 0; Indels 0; Gaps 0;
CY	9 PPTTTPPSPKPS 19
DB	4 KPTTTPPSPKPS 15
RESULT 15	
AAY51912	ID AAY51912 standard; peptide; 29 AA
XX	AC AC
XX	AAY51912;
DT	16-JUN-2000 (first entry)
XX	
DE	Basic peptide NST301.
KW	NST300, anticoagulant; thrombolytic; antianemic; dermatological; immunosuppressive; antiinflammatory; anionic phospholipid treatment; prothrombinase complex; apf is well, p-acylant activities; CMLA; cell membrane lipid asymmetry; thrombotic; sickle cell disease; thalassemia; antiphospholipid antibody syndrome; lupus erythematosus.
OS	Unidentified.
XX	
PH	Key Location/Qualifiers
FT	Modified-site 1 /note= "residue modified by myristate group"
FT	Modified-site 29 /note= "this residue is modified by a labelling group for specific binding selected among biotin and a group containing a substituent selected among a fluorophore, a radioligand and a paramagnetic contrast agent"
XX	
PN	WO2000/11026-A1
XX	
ED	02-MAP-2000
XX	
PP	23-AUG-1999; GSWO-II00456.
XX	
PP	24-AVG-1999; GSWO-II025908.
XX	
PA	(NSTN-1) NST NEUROPROTECTANT TECHNOLOGIES LTD.
XX	
EI	Ziv I., Shirvan A;
XX	
PP	WPI; 2000 23615/20.
XX	
WT	Novel basic lipids, useful e.g. for treating neurodegenerative diseases and for detecting apoptosis, contains terminal prenyl or fatty acid residue and binds to exposed cell membrane lipid -
XX	
PS	Claim 17; Page 75; 70pp; English
XX	
CC	This invention describes novel basic peptides, substituted by a prenyl or fatty acid residues, designated NSTn compounds (n) and their functional equivalents. NSTn compounds have the formula X1-(X3)n-a/(X4)b, where X1 = H; locally unsaturated C200 fatty acid residue or cysteine bound through a thioether bond to a C200 prenyl residue, linked to the rest of (n) through an amide bond; X2 = 1-6 amino acids (aa), with at least one being positively charged and any others

Db	1	KKKEEFSSEKES 12
RESULT 14		
AAAY51910		
ID	AAAY51910	standard, peptide; 28 AA.
AC	AAAY51910;	
XX		
XX	15-JUN-2000	(first entry)
XX		
XX	Basic peptide NST360.	
DE		
XX	NST360: anticoagulant, thrombolytic, antitumor, dermatological;	
XX	immunosuppressive; antiinflammatory; anionic phospholipid; treatment;	
XX	prothrombinase complex; apoptotic cell; procoagulant activity; CWLA,	
XX	cell membrane lipid asymmetry; thrombosis, sickle cell disease;	
XX	thalassemia, antiphospholipid antibody syndrome, lupus erythematosus.	
XX		
OS	Unidentified.	
XX		
XX	Key	Location/Qualifiers
XX	Modified-site 1	
PT		/note= "residue modified by myristate group"
PT	Modified-site 28	
PT		/note= "this residue is modified by a labelling group for specific binding selected among biotin and a group containing a substituent selected among a fluorescein, a radio-isotope and a paramagnetic contrast agent"
XX		
XX	W2000011026-AI.	
XX		
XX	02-MAR-2000.	
XX		
XX	24-AUG-1999;	99WH-1100454.
XX		
XX	24-AUG-1999;	9811-0125008.
XX		
PA	(NOTE) NST NEURO-SURVIVAL TECHNOLOGIES LTD	
XX		
XX	Ziv I, Shirvan A;	
PI		
XX	WPI; 2000 247615/20.	
XX		
XX	Novel basic peptide, useful e.g. for treating prothrombotic states and for detecting apoptosis, contains terminal prenyl or fatty acid residue and binds to exposed cell membrane lipid -	
XX	Disclosure: Page 74; 7pp; English.	
XX		
XX	This invention describes novel basic peptides, substituted by a prenyl or fatty acid residue, designated NST360 compounds (I) and their functional equivalents. NST360 compounds have the formula	
CC	X1 (X3)2(X4)2, where X1 especially unsaturated C-200 fatty acid residue or cysteine bound through a thioether bond to a 5-20C prenyl	
CC	residue, linked to the rest of (I) through an amide bond, X3 - 1-6 amino acids (aa), with at least one being positively charged and any others	
CC	being polar and uncharged, X4 = 1-6 aa, with 1 or 2 being aromatic and the others polar uncharged or hydrophobic and aliphatic; a and b = 1-8;	
CC	and X1 and X4 are located at various places in (I). The products of the invention have anticoagulant, thrombolytic, antitumor, dermatological,	
CC	immunosuppressive and antiinflammatory activity. (I) bind to anionic phospholipids which catalyze assembly of the prothrombinase complex and	
CC	are expressed by apoptotic cells. (I) are used to treat or prevent prothrombotic states in conditions associated with excessive	
CC	procoagulant activity, initiated or propagated by loss of cell membrane prenyl asymmetry (CWLA). Particularly arterial or venous thrombosis,	
CC	sickle cell disease, thalassemia, antiphospholipid antibody syndrome,	
CC	lupus erythematosus, shed membrane particles and apoptosis. (I) are also used to diagnose the loss of CWLA by detecting or imaging cell death; especially for diagnosis of thrombosis and prothrombotic states or	
CC	apoptosis-associated conditions as e.g. monitoring response to cancer	

1 2 aa, with 1 or 2 other aromatic and
hydrophobic amino acids (a and b e 1-8,
various places in the products of the
catalytic, antineoplastic, hematological,
immunomodulatory, and antitumor activity
activity of the proteinase complex and
also, are used to treat or prevent
conditions associated with excessive
and/or propagated by loss of cell membrane
cellular arterial or venous thrombosis,
via, antiphospholipid antibody syndrome,
transfusions and apoplexias. (2) are also
used by detecting or treating cell death,
tumor and proteinase inhibitors or
as a monitoring response to cancer
treatment, and monitoring drug survival after
as the delivery drugs to tissues affected by
search into the tissue via, in vivo or
assess the peptide Nucleoside, Nucleol and
the method of the invention.

1000-200 DB 214-913-39
1000-200 DB 214-913-39
Misses 1000-200 DB 214-913-39
Gaps 0

1000-200 DB 214-913-39



CC The present peptide sequence represents a specifically claimed membrane
CC binding element. The invention relates to a soluble derivative (A) of a
CC soluble polypeptide (1), which comprises at least 2 heterologous
CC membrane-binding elements (MBE) of low membrane affinity covalently
CC associated with (1). MBE interact, independently and with thermodynamic
CC additivity, with components of cellular or artificial membranes exposed
CC to extracellular fluids. (A) are used to treat disorders treatable with
CC (1) itself, specifically inflammation or any other complement-related
CC disorder (e.g. neurological disease, graft rejection, myocardial
CC infarction, sepsis, rheumatoid arthritis and many others, including
CC application to indwelling devices) and thrombolytic disease, but also to
CC treat allergy, induce weight loss, to treat ischaemia or asthma and as
CC immuno-modulators for treating multiple sclerosis. (A) are administered
CC orally, topically, by injection or inhalation at 0.01-10 (preferably
CC 0.1-10) mg/kg/day.

CC Sequence 17 AA;
Query Match 100.0%; Score 41; PP 19; Length 17;
Best Local Similarity 100.0%; Pos. No. 1-16-05; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSSKSPSPKPKPKPKPK 16
|||||
Db 1 GSSKSPSPKPKPKPKPK 16

RESULT 6
ID AAW45891 standard; peptide; 17 AA.

AC AAW45891;

XX 30-JUN-1998 (first entry)

DE Peptide membrane binding element.

XX Membrane binding element; thrombotic disease, soluble protein.

KW Complement related disease, integral membrane protein, inflammation.

XX Synthetic.

XX WC5802454-Aa.

PN 20 JAN 1998.

XX 08-JUL-1997; 97WO-BP03715.

XX 15-JUL-1996; 96GB-0014871.

XX (ADPR-) ADPROTECH PLC.

XX Dodd I, Mossakowska DEI, Smith RAG,

XX WPI; 1998-110524/10

XX Derivatives of soluble polypeptide(s) bonded to low affinity
PT membrane binding groups - useful for treating complement related and
PT thrombotic diseases, providing improved localisation at cellular
PT membranes

XX Claim 21, page 71, 75pp, English.

CC The present peptide sequence represents a specifically claimed membrane
CC binding element. The invention relates to a soluble derivative (A) of a
CC soluble polypeptide (1), which comprises at least 2 heterologous
CC membrane-binding elements (MBE) of low membrane affinity covalently
CC associated with (1). MBE interact, independently and with thermodynamic
CC additivity, with components of cellular or artificial membranes exposed
CC to extracellular fluids. (A) are used to treat disorders treatable with
CC (1) itself, specifically inflammation or any other complement-related
CC disorder (e.g. neurological disease, graft rejection, myocardial
CC infarction, sepsis, rheumatoid arthritis and many others, including

CC application to indwelling devices) and thrombolytic disease, but also to
CC treat allergy, induce weight loss, to treat ischaemia or asthma and as
CC immuno-modulators for treating multiple sclerosis. (A) are administered
CC orally, topically, by injection or inhalation at 0.01-10 (preferably
CC 0.1-10) mg/kg/day.

CC Sequence 17 AA.

Query Match 100.0%; Score 41; PP 19; Length 17;

Best Local Similarity 100.0%; Pos. No. 1-16-06; Indels 0; Gaps 0;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSSKSPSPKPKPKPKPK 16
|||||
Db 1 GSSKSPSPKPKPKPKPK 16

RESULT 7

AA826818

ID AAP26818 standard; peptide; 17 AA.

AC AAB26818;

XX 23-JAN 2001 (first entry)

DE Membrane targeted complement inhibitor peptide.

XX Cation perfuser, transferrin, storage, anti-inflammatory;

KW immunosuppressive, vasotropic, complement activation inhibitor;

XX allergic rejection; ischaemia reperfusion injury.

XX Synthetic.

XX Key Location/Qualifiers

XX Modified-site 17

XX /note- "C-terminal Cys forms a disulphide bond with the

XX W02000053007-A1

XX 14-SEP-2000.

XX 09-MAP 2000; 2000WO-0200834.

XX 10-MAP-1999; 99GB-0005503.

XX (ADPR-) ADPROTECH LTD.

XX Smith RAG, Pratt JP, Sacks SH;

XX WPI; 2000 601900/57.

XX Preparation for perfusing organ prior to transplantation or storage
PT comprises soluble derivative of a soluble polypeptide which comprises
PT two heterologous membrane binding elements with low membrane affinity
PT -
XX Example 1; Page 49, 47pp, English.

CC The present invention relates to formulations and preparations for
CC perfusing an organ prior to transplantation or storage. The preparation
CC comprises a soluble derivative of a polypeptide, which has two or more
CC heterologous membrane binding elements, the membrane binding elements are
CC capable of interaction, independently and with thermodynamic additivity,
CC with membrane components of the organ exposed to extracellular perfusion
CC fluids, and a flush storage solution. The preparation exhibits
CC anti-inflammatory, immunosuppressive and vasotropic activity and works as
CC a complement activation inhibitor and an inhibitor of white blood
CC lymphocyte activity. The preparation is used for preparing an organ prior
CC to transplantation or storage and for prevention treatment or
CC amelioration of a disease or disorder associated with inflammation,
CC inappropriate complement activation or inappropriate activation of
CC coagulant or thrombotic processes prior to, during or after

in brain. The present invention is useful for allograft rejection and transplanted organs failure, ischaemic necrosis, radiation injury in carcinoma and various graft rejection. The peptide targeted membrane inhibitor for the preparation of the invention.

Query Match 100.0%; Score 81; DB 21; Length 17;
Best Local Similarity 100.0%; Pred. No. 13e 56;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

AA

in anti-angiogenic peptide.

inhibitor; membrane binding element;

17

17

17; 100% VF;

Antibacterial polypeptide useful for
treatment of bacterial infections, containing a polypeptide attached
to a carrier.

17

The present invention describes an antibacterial compound (I), comprising a conjugate of glycerophosphate and peptide (II), and a carrier (III). (I) comprises the formula V-L-W-X, where V = a glycopeptide moiety that inhibits protein synthesis in bacteria, W = a linking group, X = a peptidic membrane-associating element, and Y = H or a moiety insertable element. Also described is a method of treating or preventing a bacterial infection, comprising the administration of (I) and (II) of (I) in the manufacture of a medicament for the treatment or prevention of a bacterial infection. (II) are used in the manufacture of a medicament for the treatment or prevention of a bacterial infection in a human or animal body, including both the gram positive and gram negative bacteria including Mycobacterium sp., Pseudomonas sp., Escherichia sp., Staphylococcus sp., Vibrio sp., Neisseria sp., Bacillus sp., Klebsiella sp., Hemophilus sp., Clostridium sp., Penicillium sp., Aspergillus sp., Pneumococcus sp. or Salmonella sp., particularly antibiotic-resistant bacterial strains. (I) are also useful as wound treatment agents to prevent adhesion of bacteria to matrix proteins, especially fibrinogen, exposed in wound tissue; and for prophylactic use in dental treatment as

an alternative to, or in conjunction with, antibiotic prophylaxis. (1) has stronger binding to bacterial membranes which have a higher potential for antibiotic resistance than the eukaryotic organisms, also having a higher penetration of membrane associated biosynthetic proteins. Vancomycin shows an enhanced antimicrobial activity upon derivatization with (1) and is effective to treat the antibiotic resistant bacterial strains. ABB81234 to ABB81235 represent peptides given in the exemplification of the present invention.

XX Sequence 17 AA;

Query Match 100.0%, Score 61, Gap 0, Length 17;
Best Local Similarity 100.0%, Pred. No. 13e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSSKSPSKYKXKPGD 16
DB 1 GSSKSPSKYKXKPGD 16

RESULT 10
ABB07533
ID ABB07533 standard; pep1 (de); 17 AA.
XX AC ABB07533;
XX DT 22 APR 2002 (first entry)
XX DE Amino acid sequence of APT542.
XX KW CD59; lipid raft derivative; NAF; neuroprotective; nontropic; human; cerebroprotective; antiplatelet; antiplatelet; antitumor; cardiac; antiproliferative; antineoplastic; dermatological; hypertensive; vasotropic; antirheumatic; antiarthritic; antiinflammatory; ophthalmological; immunosuppressive; antianemic; nephrotropic; antiinfectivity; antibacterial; antiatherosclerotic; vulnery.

XX OS Synthetic.
XX OS Homo sapiens.

XX FH Key Location/Qualifiers
FT Modified-site 1 /note= "B myristoyl"
FT Modified-site 17 /note= "C-terminal 2-thiopyridyl-OR2"
XX KW CD59; 4-9 AA.
XX PD 17-JAN-2002.
XX PF 06-JUL 2001, 2001W03504867.
XX PR 07-JUL 2000, 2000JP 0026024.
XX PA (ADPR-) ADPR07533 LTD.
XX PI Rowling PJE, Smith GP, Ridley SH;
XX WPI; 2002 164846/21.
XX DR
XX PT Lipid raft targeted derivative of a soluble polypeptide 4-9, a soluble complement regulatory molecule for treating disorders involving
PT Complement activity and various inflammatory, immunological and immune disorders
XX PI
XX XX
XX Example 1, Page 43, 51pp, English.
XX CC The invention relates to a soluble derivative (1) of a soluble polypeptide (17) has two or more heterogeneous membrane binding elements with low membrane affinity devalently associated with the polypeptide, the elements being capable of interacting with components of cellular or artificial membranes exposed to extracellular fluids and target lipid raft components of membrane. (1) is useful for treating disorders

amenable to treatment by a soluble peptide fragment of CD59, NAF or other therapeutic agent, and for the preparation of a medicament for treatment of disorders involving complement activity and various inflammatory and immune disorders. (1) is useful for treating neurological disorders (e.g. multiple sclerosis, stroke, Parkinson's, Alzheimer's disease, traumatic brain injury and allergic encephalitis), disorders of inappropriate or undesirable complement activation (e.g. xenograft rejection, corneal graft rejection), inflammatory disorders (including ulcerative colitis, Crohn's disease, uveitis, psoriasis, asthma, scleroderma, acute pancreatitis), post-ischemic reperfusion conditions (e.g. myocardial infarction, hypertension, renal ischaemia, restenosis, atherosclerosis), infectious diseases or sepsis (e.g. multiple organ failure, septic shock), autoimmune diseases (e.g. rheumatoid arthritis, systemic lupus erythematosus, hemolytic anemia, glomerulonephritis and myasthenia gravis), reproductive disorders (antibody or complement mediated infertility), and wound healing. The present sequence represents the amino acid sequence of APT542, used in the synthesis of a lipid raft targeted derivative of soluble human urinary CD59 (APT532).

XX Sequence 17 AA;

Query Match 100.0%, Score 61, Gap 0, Length 17;
Best Local Similarity 100.0%, Pred. No. 13e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSSKSPSKYKXKPGD 16
DB 1 GSSKSPSKYKXKPGD 16

RESULT 11
ABB81235
ID ABB81235 standard; peptide; 17 AA
XX AC ABB81235;
XX DT 20 AVG 2002 (first entry)
XX DE Antibacterial peptide SEQ ID NO:2.
XX KW Antibacterial; glycopeptide; peptidic membrane associating element; bacterial infection; vancomycin; peptidoglycan biosynthesis inhibition; antibiotic.
XX OS Synthetic.
XX KW WQ00036612-A1.
XX PD 10 MAY 2002.
XX PF 02 NOV 2001; 2001W03504867.
XX PR 02 NOV 2000; 2000JP 0026024.
XX PA (UYCA) UNIV CAMBRIDGE TECH SERVICES LTD.
XX PI (ADPR-) ADPR07533 LTD.
XX PI Cooper MA, Betley JR,
XX WPI; 2002-471408/50.
XX DR
XX PT Antibacterial compound, useful for the treatment of a bacterial infection by a gram positive or negative bacteria, comprising a conjugate of glycopeptide and peptidic membrane associating element
XX PI
XX Example 4; Page 52; 64pp; English.
XX CC The present invention describes an antibacterial compound (1), comprising a conjugate of glycopeptide and peptidic membrane associating elements. (1) comprises the formula V-P-W-X, where: V = a glycopeptide moiety that inhibits peptidoglycan biosynthesis in bacteria; P = a linking group; W = a peptidic membrane associating element; and X = H or a membrane insertive element. Also described: (1) a method of treating or preventing

the administration of (1) and (2) use
a medicament for the treatment or prevention
of a bacterial infection in a human or
animal, comprising a peptide which is
gram positive and transmembrane bacteria
such as *Staphylococcus* sp., *Enterococcus* sp.,
Streptococcus sp., *Micrococcus* sp.,
Listeria sp., *Yersinia* sp., *Klebsiella*
sp., *Pseudomonas* sp., *Acinetobacter* sp.,
and *Mycobacterium* sp., particularly antibiotic resistant
strains, as wound treatment agents to
prevent infection, especially fibroblast
infection with antibiotic prophylaxis
and/or treatment of bacterial infections
in membranes which have a higher
permeability than the extracellular matrix, also
membrane associated periplasmic proteins,
the antibiotic resistance bacterial
represent peptides shown in the
invention.

Query 5: CB 21; Score 58;
Best Local Similarity 100.0%; Pred.No. 0.967;
Matches 11; Conservative 0; Mismatches 0; Gaps 0;

AA

BB

the storage, administration of
the complement activation inhibitor
in a perfusion injury

BB

Query 5: Myristoyl; Score 58;

Query 5: 2 Thiopyridyl; Score 58;

BB

in prior to transmembrane or storage
if a soluble polypeptide which comprises
the elements with low membrane affinity

Example 2; Page 20; 47pp; English.

The present invention relates to foundations and preparations for
perfusing an organ prior to transplantation or storage. The preparation
comprises a soluble derivative of a polypeptide, which has two or more
heterologous membrane binding elements. The membrane binding elements are
capable of interacting, independently and with thermodynamic affinity,
with membrane components of the organ exposed to extracellular perfusion
fluids, and a flush storage solution. The preparation exhibits
anti-inflammatory, immunosuppressive and vasodilatory activity and a low
lymphocytic activity. The preparation is used for preparing an organ prior
to transplantation or storage and for prevention, treatment or
amelioration of a disease or disorder associated with inflammation,
injury or thrombotic processes prior to, during or after
transplantation or storage of an organ. The preparation is useful for
treating hyperacute and acute allograft rejection of transplanted organs
such as kidney, heart, liver or lungs, ischaemia-reperfusion injury in
transplanted organs, xenograft rejection and corneal graft rejection. The
present sequence represents a peptidic membrane binding element used in
an example of the preparation of the invention.

Sequence 20 AA;

Query Match 69.9%; Score 58; PB 21; Length 27;
Best Local Similarity 100.0%; Pred.No. 0.967;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 SPSKVKKVKPG 15
DB 2 SPSKVKKVKPG 12

RESULT 13

AAO03872
ID AAO03872 standard; Protein; 83 AA.

AC AAO03872;

DT C6-NCV-2001 (first entry)

DE Human polypeptide SEQ ID NO 17764.

XX Human, myokine, cell proliferation, cell differentiation, bone therapy;
XX vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
XX tissue growth factor; immunomodulatory; cancer; leukaemia;
XX nervous system disorders; arthritis; inflammation.

OS Homo sapiens.

PN W0200164935-A2.

PD 07-SEP-2001.

PF 26-FEB-2001; C61W; US-920.

PR 28-FEB-2000; 2000US-051126.

PR 18-MAY-2000; 2000US-057409.

PA (HYSE-) HYSEQ INC.

PI Tang YT, Liu C, Drmanac RT;

DR WPI; 2001-514935/56.

DR N-PSDB; AA183803.

XX Isolated nucleic acids and polypeptides, useful for preventing
XX diagnosing and treating e.g. leukaemia, inflammation and immune
XX disorders.

PS Claim 20; SEQ ID NO 17764; 1399pp + Sequence listing; English.

QY 1 GSSGSPSXXXXX 13
|||:|||||
Db 106 GSSPNPXXXXX 118

Search completed: March 3, 2003, 10:18:17
Job time : 29.878 secs

DB 145 SPSNETBKKKZPPSPKYS 163
 |||||

RESULT 2

US-08-405-175A-6

Sequence 6, Application US/08405175A
 Patent No. 5885772
 GENERAL INFORMATION:
 APPLICANT: Aderem, Alan A.
 APPLICANT: Chen, Jianmin
 APPLICANT: Chang, Sandy
 TITLE OF INVENTION: METHOD FOR THE DETECTION OF AMENGEHALY
 NUMBER OF SEQUENCES: 12
 CORRESPONDENCE ADDRESS:

ADDRESSEE: Klauter & Jackson
 STREET: 411 Hackensack Avenue
 CITY: Hackensack
 STATE: New Jersey
 COUNTRY: USA

ZIP: 07601

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08405175A
 FILING DATE: 16-MAR-1995
 CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Jack E. Ehl, David A.

REGISTERED NUMBER: 26,742

REFERENCE/AGENT NUMBER: 435 1 121A

TELECOMMUNICATION INFORMATION:

TELEPHONE: 201 487-5800

TELEFAX: 201 343-1684

TELEX: 133521

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 335 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

DESCRIPTION: Predicted primary structure of human WAPK5

HYPOTHETICAL: NO

US-08-405-175A-6

Query Match 94.2%, Score 98, DP 2, Length 335,

Best Local Similarity 100.0%, Freq. NO, 7.3e 07,

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 144 SPSNETBKKKZPPSPKYS 162

|||||

RESULT 3

US-08-405-175A-7

Sequence 7, Application US/08405175A

Patent No. 5885772

GENERAL INFORMATION:

APPLICANT: Aderem, Alan A.

APPLICANT: Chen, Jianmin

APPLICANT: Chang, Sandy

TITLE OF INVENTION: METHOD FOR THE DETECTION OF AMENGEHALY

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:

ADDRESSEE: Klauter & Jackson

STREET: 411 Hackensack Avenue

CITY: Hackensack

STATE: New Jersey

ZIP: 07601

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08405175A

FILING DATE: 16-MAR-1995

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Jack E. Ehl, David A.

REGISTERED NUMBER: 26,742

REFERENCE/AGENT NUMBER: 435 1 121A

TELECOMMUNICATION INFORMATION:

TELEPHONE: 201 487-5800

TELEFAX: 201 343-1684

TELEX: 133521

COUNTRY: USA

ZIP: 07601

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08405175A

FILING DATE: 16-MAR-1995

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Jack E. Ehl, David A.

REGISTERED NUMBER: 26,742

REFERENCE/AGENT NUMBER: 435 1 121A

TELECOMMUNICATION INFORMATION:

TELEPHONE: 201 487-5800

TELEFAX: 201 343-1684

TELEX: 133521

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 309 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

DESCRIPTION: Predicted primary structure of human WAPK5

HYPOTHETICAL: NO

US-08-405-175A-7

Query Match 94.2%, Score 97, DP 2, Length 309,

Best Local Similarity 100.0%, Freq. NO, 3.4e 06,

Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

DB 139 SPSNETBKKKZPPSPKYS 156

|||||

RESULT 4

US-08-405-175A-8

Sequence 8, Application US/08405175A

Patent No. 5885772

GENERAL INFORMATION:

APPLICANT: Aderem, Alan A.

APPLICANT: Chen, Jianmin

APPLICANT: Chang, Sandy

TITLE OF INVENTION: METHOD FOR THE DETECTION OF AMENGEHALY

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:

ADDRESSEE: Klauter & Jackson

STREET: 411 Hackensack Avenue

CITY: Hackensack

STATE: New Jersey

COUNTRY: USA

ZIP: 07601

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08405175A

FILING DATE: 16-MAR-1995

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Jack E. Ehl, David A.

REGISTERED NUMBER: 26,742

REFERENCE/AGENT NUMBER: 435 1 121A

TELECOMMUNICATION INFORMATION:

TELEPHONE: 201 487-5800

TELEFAX: 201 343-1684

TELEX: 133521

? OPERATING SYSTEM: Windows 95
 ? SOFTWARE: FastSeq for Windows Version 2.0b
 ? CURRENT APPLICATION DATA: US/09-018-253
 ? APPLICATION NUMBER: US/09-018-253
 ? FILING DATE: 14-MAR-1997
 ? FILER APPLICATION DATA
 ? APPLICATION NUMBER
 ? FILING DATE:
 ? ATTORNEY/AGENT INFORMATION:
 ? NAME: Baile, Ph D., Lisa A.
 ? REGISTRATION NUMBER: 28,147
 ? REFERENCE/AGENT NUMBER: 07/07/94-001
 ? TELECOMMUNICATION INFORMATION:
 ? TELEPHONE: 615/678-5070
 ? TELEFAX: 615/678-5030
 ? INFORMATION FOR SEQ ID NO: 1:
 ? SEQUENCE: HAPA-TEP-11
 ? LENGTH: 25 amino acids
 ? TYPE: amino acid
 ? TOPOLOGY: linear
 ? MOLECULE TYPE: Peptide
 ? US 09-018-253-25

Query Match: 57.7%, Score 60, EP 4, Length 25;
 Best Local Similarity: 100.0%, Pred. No. 0.018;
 Matches: 12, Conservative: 0, Mismatches: 0, Indels: 0, Gaps: 0;

CQ 9 KKKKKKKKKKKK 19
 DB 1 KKKKKKKKKKKK 12

RESULT 8

US-09-018-253 25
 ? Sequence 25, Application US/09-018-253B

? GENERAL INFORMATION:
 ? APPLICANT: Tsien, Roger Y.
 ? APPLICANT: Miyawaki, Atsushi
 ? TITLE OF INVENTION: FLUORESCENT PROTEIN SENSORS FOR
 ? TITLE OF INVENTION: DETECTION OF ANAESTHESIA
 ? FILE REFERENCE: 07257/042001
 ? CURRENT APPLICATION NUMBER: US/09-018-253B
 ? CURRENT FILING DATE: 1997-03-14
 ? NUMBER OF SEQ ID NOS: 14
 ? SOFTWARE: FastSeq for Windows Version 4.0
 ? SEQ ID NO: 26
 ? LENGTH: 25
 ? TYPE: PPT
 ? ORGANISM: Rattus norvegicus
 ? US-09-018-253 25

Query Match: 57.7%, Score 60, EP 4, Length 25;
 Best Local Similarity: 100.0%, Pred. No. 0.018;
 Matches: 12, Conservative: 0, Mismatches: 0, Indels: 0, Gaps: 0;

CQ 9 KKKKKKKKKKKK 19
 DB 1 KKKKKKKKKKKK 12

RESULT 9

US-08-842 322 20
 ? Sequence 20, Application US/08-042-322

? GENERAL INFORMATION:
 ? APPLICANT: Persechini, Anthony
 ? TITLE OF INVENTION: SELECTION BY FEET CHANGES OF LIGAND
 ? TITLE OF INVENTION: BINDING BY GFE FOR THE PROTEINS
 ? NUMBER OF SEQUENCES: 33
 ? CORRESPONDENT ADDRESS:
 ? ADDRESS: NIXON, HARGRAVE, DEVANS & DOYLE LLP
 ? STREET: Clinton Square, P.O. Box 1051

? CITY: Rochester
 ? STATE: New York
 ? COUNTRY: USA
 ? ZIP: 14603
 ? COMPUTER READABLE FORM:
 ? MEDIUM TYPE: floppy disk
 ? OPERATING SYSTEM: PC-DOS/MS-DOS
 ? SOFTWARE: Release 4.0, Version #1.30
 ? CURRENT APPLICATION DATA:
 ? APPLICATION NUMBER: US/09-042-322
 ? FILING DATE:
 ? CLASSIFICATION: 43C
 ? ATTORNEY/AGENT INFORMATION:
 ? NAME: BERMAN, SUSAN J.
 ? REGISTRATION NUMBER: 34,103
 ? REFERENCE/AGENT NUMBER: 17/06/170
 ? TELECOMMUNICATION INFORMATION:
 ? TELEPHONE: 715 263-1636
 ? TELEFAX: 715 263-1600
 ? INFORMATION FOR SEQ ID NO: 20
 ? SEQUENCE CHARACTERISTICS:
 ? LENGTH: 25 amino acids
 ? TYPE: amino acid
 ? STRANDEDNESS: N/A relevant
 ? TOPOLOGY: linear
 ? MOLECULE TYPE: Peptide
 ? US-09-042-322-20

Query Match: 57.7%, Score 60, EP 4, Length 25;
 Best Local Similarity: 100.0%, Pred. No. 0.018;
 Matches: 12, Conservative: 0, Mismatches: 0, Indels: 0, Gaps: 0;

CQ 8 KKKKKKKKKKKK 19
 DB 1 KKKKKKKKKKKK 12

RESULT 10

US-09-316-919-42
 ? Sequence 42, Application US/09-316-919

? GENERAL INFORMATION:
 ? APPLICANT: Tsien, Roger Y.
 ? APPLICANT: Baird, Geoffrey
 ? TITLE OF INVENTION: FLUORESCENT PROTEIN INDICATORS
 ? FILE REFERENCE: 07257/073001
 ? CURRENT APPLICATION NUMBER: US/09-316-919
 ? CURRENT FILING DATE: 1999-05-21
 ? NUMBER OF SEQ ID NOS: 63
 ? SOFTWARE: FastSeq for Windows Version 4.0
 ? SEQ ID NO: 42
 ? LENGTH: 25
 ? TYPE: PPT
 ? ORGANISM: Rattus norvegicus
 ? US-09-316-919-42

Query Match: 57.7%, Score 60, EP 4, Length 25;
 Best Local Similarity: 100.0%, Pred. No. 0.018;
 Matches: 12, Conservative: 0, Mismatches: 0, Indels: 0, Gaps: 0;

CQ 8 KKKKKKKKKKKK 19
 DB 1 KKKKKKKKKKKK 12

RESULT 11

US-89-405 175A-4
 ? Sequence 4, Application US/89-405175A

? GENERAL INFORMATION:
 ? APPLICANT: Aderem, Alan A.
 ? APPLICANT: Chen, Jianmin
 ? TITLE OF INVENTION: SELECTION BY FEET CHANGES OF LIGAND
 ? TITLE OF INVENTION: BINDING BY GFE FOR THE PROTEINS
 ? NUMBER OF SEQUENCES: 33
 ? CORRESPONDENT ADDRESS:
 ? ADDRESS: NIXON, HARGRAVE, DEVANS & DOYLE LLP
 ? STREET: Clinton Square, P.O. Box 1051

RESULT 12

US-08-842 322 20
 ? Sequence 20, Application US/08-042-322

? GENERAL INFORMATION:
 ? APPLICANT: Persechini, Anthony
 ? TITLE OF INVENTION: SELECTION BY FEET CHANGES OF LIGAND
 ? TITLE OF INVENTION: BINDING BY GFE FOR THE PROTEINS
 ? NUMBER OF SEQUENCES: 33
 ? CORRESPONDENT ADDRESS:
 ? ADDRESS: NIXON, HARGRAVE, DEVANS & DOYLE LLP
 ? STREET: Clinton Square, P.O. Box 1051

CQ 8 KKKKKKKKKKKK 19
 DB 1 KKKKKKKKKKKK 12

RESULT 13

US-08-842 322 20
 ? Sequence 20, Application US/08-042-322

? GENERAL INFORMATION:
 ? APPLICANT: Persechini, Anthony
 ? TITLE OF INVENTION: SELECTION BY FEET CHANGES OF LIGAND
 ? TITLE OF INVENTION: BINDING BY GFE FOR THE PROTEINS
 ? NUMBER OF SEQUENCES: 33
 ? CORRESPONDENT ADDRESS:
 ? ADDRESS: NIXON, HARGRAVE, DEVANS & DOYLE LLP
 ? STREET: Clinton Square, P.O. Box 1051

2. THE DETECTION OF AN INTRUSION

11

3

100

NATIONAL OFFICIAL BOARD OF EXAMINERS

1000 14; DR 2; 1000 14;
 1000 14; DR 2; 1000 14;
 1000 14; DR 2; 1000 14;

THE N SENSE OF AWAYTES

[illegible]

1000

ATTORNEY/AGENT INFORMATION:
NAME: Haile, Ph.D., L.s.a.
REGISTRATION NUMBER: 38,347
REFERENCE/BOOKET NUMBER: 07257/04360;
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5090
TELEFAX: 619/678-5099
INFORMATION FOR SERIAL NO.: 27;
SEQUENCE CHARACTERISTICS
LENGTH: 24 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
MS-08-619-253-27

Query Match	46.08%	Score 49; DB 2; Length 34;
Best Local Similarity	90.08%	Pred. No. 0.01;
Matches	9; Conservative	1; Mismatches

Qy	Qx
18	18
17	17
16	16
15	15
14	14
13	13
12	12
11	11
10	10
9	9
8	8
7	7
6	6
5	5
4	4
3	3
2	2
1	1

```

RESULT 13
US-08-818-252-27
: Sequence 7, Application US09081852B
: Patent No. 6197928
: GENERAL INFORMATION.
:
: APPLICANT: Tsien, Roger Y.
: APPLICANT: Miyawaki, Atsushi
: TITLE OF INVENTION: FINGERPRINTS IN SEMI-CONDUCTOR
: TITLE OF INVENTION: DETECTION OF ANALYTES
: FILE REFERENCE: 0757432001
: CURRENT APPLICATION NUMBER: US 09-018-252P
: CURRENT FILING DATE: 1997-03-14
: NUMBER OF SEQ ID NOS: 56
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 27
: LENGTH: 24
: TYPE: PRT
: ORGANISM: Mus musculus
: US-08-818-252-27

```

Query Match 46.2%; Score 48; DP 4; Length 24;
Best Local Similarity 90.0%; Pred. No. 0.91;
Matches 9; Conservative 1; Mismatches 0; Index

9	KKKPESFFK	18
	:	
1	KKKKFSFFK	10

```

RESULT 14
US-08-842-322-21
? Sequence 21, Application US/08842322
? Patent No. 6176257
? GENERAL INFORMATION:
? APPLICANT: Persichini, Anthony
? TITLE OF INVENTION: DETECTION BY FREE CHARGES OF LIGAND
? TITLE OF INVENTION: DETECTION BY FREE CHARGES OF LIGAND
? NUMBER OF SEQUENCES: 33
? CORRESPONDENCE ADDRESS:
? ADDRESS: NANCY HASSEBANE, EDWARD A. LEYLA LLP
? STREET: Clinton Square, P.O. Box 195;
? CITY: Rochester
? STATE: New York
? COUNTRY: USA
? ZIP: 14603
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS

```

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? SOFTWARE: Patent In Release #1.0, Version #1.30
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/09/942,322
? FILING DATE:
? CLASSIFICATION: 436
? ATTORNEY/AGENT INFORMATION:
? NAME: BRAMAN, SUSAN J.
? REGISTRATION NUMBER: 34,103
? REFERENCE/KEY NUMBER: 17,000,000
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 716-263-1636
? TELEFAX: 716-263-1600
? INFORMATION FOR SEQ ID NO: 21:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 24 amino acids
? TYPE: amino acid
? STRANDEDNESS: not relevant
? TOPOLOGY: linear
? MOLECULE TYPE: peptide
US-09-942,322 21

```

```

Query Match 46.2%; Score 48; DB 4; Length 24;
Best Local Similarity 90.0%; Pred. No. 0.91;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 9 KKKKESKK 18
Db 1 KKKKESKK 10

```

```

RESULT 15
US 09-214-919-43
? Sequence 43, Application US/09316919
? Patent No. 6469154
? GENERAL INFORMATION:
? APPLICANT: Tshen, Roger Y.
? APPLICANT: Baird, Geoffrey
? TITLE OF INVENTION: FLUORESCENT PROTEIN INDICATORS
? FILE REFERENCE: 07257/073001
? CURRENT APPLICATION NUMBER: US/09/316,919
? CURRENT FILING DATE: 1999-05-21
? NUMBER OF SEQ ID NOS: 63
? SOFTWARE: FastSeq for Windows Version 4.0
? SEQ ID NO 43
? LENGTH: 24
? TYPE: PRT
? ORGANISM: Mus musculus
US-09-214-919-43

```

```

Query Match 46.2%; Score 48; DB 4; Length 24;
Best Local Similarity 90.0%; Pred. No. 0.91;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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```

QY 9 KKKKESKK 18
Db 1 KKKKESKK 10

```

```

Search completed: March 3, 2003, 08:15:50
Job time : 14.6829 secs

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C:Species: Volvox carteri
C>Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #extn_change 12-Jul-1993
C:Accession: JQ0795
R:Mueller, K.; Lindauer, A.; Bruederlein, M.; Schmitt, P.
Gene 93, 167-175, 1990
A:Title: Organization and transcription of Volvox basistome encoding genes, specifically
A:Reference number: JQ0794; MUID:9133924; PMID:222741
A:Accession: JQ0795
A:Molecule type: DNA
A:Residues: 1-157 <MUE>
A:Cross references: CP_M31321, MIF_3176554, EMBL:AAA42444.1; EMBL:J01974
C:Genetics:
A:Gene: H2B-III
C:Superfamily: histone H2B
C:Keywords: chromosomal protein; DNA binding; nucleosome core; nucleus

Query Match 57.38; Score 47; DP 2; Length 144;
Best Local Similarity 72.78; Pred. NO. 25;
Matches 8; Conservative 3; Mismatches 6; Indels 0; Gaps 0

QY 3 PPKKKYSPSK 13
|||||:|:|:
DB 31 PPKKKYAPAK 41

RESULT 11
VVVP2J
P: Protein VP2 Polymavirus JC
N: Contains: coat protein VP3
C:Species: Polymavirus hominis 2 (polymavirus JC)
C>Date: 22-Feb-1995 #sequence_revision 22-Feb-1995 #extn_change 12-Jul-1993
C:Accession: A03633
R:Frisque, R.D.; Bream, G.L.; Cannelia, M.T.
J. Virol. 51, 458-469, 1984
A:Title: Human polymavirus JC virus genome.
A:Reference number: A03633; MUID:8426611; PMID:6546957
A:Accession: A03633
A:Molecule type: DNA
A:Residues: 1-344 <PPI>
A:Cross references: CP_J01974, BP_32227, EMBL:V01114, EMBL:AA0206.1; E
C:Superfamily: polymavirus coat protein VP2
C:Keywords: late protein
F120244/Protein: coat protein VP2 #status predicted:VP2

Query Match 57.38; Score 47; DP 1; Length 344;
Best Local Similarity 61.18; Pred. NO. 25;
Matches 11; Conservative 1; Mismatches 4; Indels 0; Gaps 1

CY 1 DGPPTFF--PFSPPSPSP 16
|||||:|:|:
DB 415 PPNPPPPPPPPPPASPP 142

RESULT 12
T00698
methionyl aminopeptidase (EC 3.4.11.18) P6E1331 - Arabidopsis thaliana
N:Alternate names: translation initiation factor eIF2 associated protein
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 01-Feb-1993 #sequence_revision 01-Feb-1993 #extn_change 12-Jul-1993
C:Accession: T00698; D04875
R:Bounslay, S.D.; Kaul, S.; Lin, X.; Vetchur, K.A.; Crosby, M.A.; Brand, N.; Bounslay, S.
submitted to the EMBL Data Library, June 1998
A:Description: Arabidopsis thaliana chromosome 11 BAC P6E13 genomic sequence
A:Reference number: Z14180
A:Accession: T00698
A>Status: translated from GR/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-431 <ROU>
A:Cross references: EMBL:AC004005; MIF:93212846; EMBL:AA023422.1; EMBL:J012971
A:Experimental source: cultivar Columbia
R:Lin, X.; Kaul, S.; Bounslay, S.D.; Shea, T.P.; Boudig, M.; Tatem, C.; Boudig, M.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.; Bounslay, S.; Boudig,
euss, D.; Nierman, W.C.; White, O.; Eisen, C.A.; Salzberg, S.L.; Fraser, J.C.; Boudig,

Validated - EMBL
Accession: JQ0795
Gene 93, 167-175, 1990
A:Title: Organization and transcription of Volvox basistome encoding genes, specifically
A:Reference number: JQ0794; MUID:9133924; PMID:222741
A:Accession: JQ0795
A:Molecule type: DNA
A:Residues: 1-157 <MUE>
A:Cross references: CP_M31321, MIF_3176554, EMBL:AAA42444.1; EMBL:J01974
C:Genetics:
A:Gene: H2B-III
C:Superfamily: histone H2B
C:Keywords: chromosomal protein; DNA binding; nucleosome core; nucleus

Query Match 57.38; Score 47; DP 2; Length 144;
Best Local Similarity 72.78; Pred. NO. 14;
Matches 8; Conservative 3; Mismatches 6; Indels 0; Gaps 0

QY 3 PPKKKYSPSK 13
|||||:|:|:
DB 31 PPKKKYAPAK 41

RESULT 11
VVVP2J
P: Protein VP2 Polymavirus JC
N: Contains: coat protein VP3
C:Species: Polymavirus hominis 2 (polymavirus JC)
C>Date: 22-Feb-1995 #sequence_revision 22-Feb-1995 #extn_change 12-Jul-1993
C:Accession: A03633
R:Frisque, R.D.; Bream, G.L.; Cannelia, M.T.
J. Virol. 51, 458-469, 1984
A:Title: Human polymavirus JC virus genome.
A:Reference number: A03633; MUID:8426611; PMID:6546957
A:Accession: A03633
A:Molecule type: DNA
A:Residues: 1-344 <PPI>
A:Cross references: CP_J01974, BP_32227, EMBL:V01114, EMBL:AA0206.1; E
C:Superfamily: polymavirus coat protein VP2
C:Keywords: late protein
F120244/Protein: coat protein VP2 #status predicted:VP2

Query Match 57.38; Score 47; DP 1; Length 344;
Best Local Similarity 61.18; Pred. NO. 25;
Matches 11; Conservative 1; Mismatches 4; Indels 0; Gaps 1

CY 1 DGPPTFF--PFSPPSPSP 16
|||||:|:|:
DB 415 PPNPPPPPPPPPPASPP 142

RESULT 12
T00698
methionyl aminopeptidase (EC 3.4.11.18) P6E1331 - Arabidopsis thaliana
N:Alternate names: translation initiation factor eIF2 associated protein
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 01-Feb-1993 #sequence_revision 01-Feb-1993 #extn_change 12-Jul-1993
C:Accession: T00698; D04875
R:Bounslay, S.D.; Kaul, S.; Lin, X.; Vetchur, K.A.; Crosby, M.A.; Brand, N.; Bounslay, S.
submitted to the EMBL Data Library, June 1998
A:Description: Arabidopsis thaliana chromosome 11 BAC P6E13 genomic sequence
A:Reference number: Z14180
A:Accession: T00698
A>Status: translated from GR/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-431 <ROU>
A:Cross references: EMBL:AC004005; MIF:93212846; EMBL:AA023422.1; EMBL:J012971
A:Experimental source: cultivar Columbia
R:Lin, X.; Kaul, S.; Bounslay, S.D.; Shea, T.P.; Boudig, M.; Tatem, C.; Boudig, M.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.; Bounslay, S.; Boudig,
euss, D.; Nierman, W.C.; White, O.; Eisen, C.A.; Salzberg, S.L.; Fraser, J.C.; Boudig,

Best Overall Similarity: 69.00, Ident: 60, Mismatches: 40, Indels: 0, Gaps: 0;
 Matches: 117, Conservative: 17, Mismatches: 40, Indels: 0, Gaps: 0;
 QY 1 DGPYKPKKPKKPKSKK 16
 ||||| ||||| |||||
 DE 40 DGPYKPKKPKKPKSKK 107

RESULT 2

HC H2B4_V11-A STANFORD, FET, 150 AA.
 AC P16868;
 DT 01-NOV-1997 (Pel 16, last sequence update)
 DT 01-NOV-1997 (Pel 16, last sequence update)
 DT 16 OCT 2001 (Pel 40, last annotation update)
 DE HISTONE H2B-IV.
 CS Volvox carterii.
 CC Eukaryota; Metazoa; Embodiment; Eukaryota; Embodiment; Volvocales;
 CC Volvocales; Volvox
 OX NCBI_TaxID=1067;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=I. Nagaiensis / H107;
 RV Meyer, R. A., Lindner, A., Rindler-Schjerve, P.,
 RA Mueller, K., Lindner, A., Rindler-Schjerve, P.,
 RT "Organization and transcription of Volvox carterii genes:
 RT similarities between algal and animal genes."
 RL Gene 93167-175 (1990).
 CC -1- SUBMITTER: THE NATURE OF AN ORGANISM CONTAINING TWO MOLECULES OF
 CC H2A, H2B, H2, AND H4, WHICH WRAP APPROXIMATELY 146 BP OF DNA.
 CC -1- SUBCELLULAR LOCATION: Nuclear.
 CC -1- SIMILARITY: BELONGS TO THE HISTONE H2B FAMILY.

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 CC between the Swiss Institute of Bioinformatics and the EMBL Data Bank.
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 CC or send an email to license@sib-sib.ch).

CC EMBL: M16822; AAA4250.1;
 CC FET: M00737; M00737;
 CC InterPro: IPR000558; Histone H2B
 CC InterPro: IPR004822; Histone_core.
 CC Pfam: PF00001; Histone_H2B.
 CC PRINTS: PR00001; HISTONE_H2B.
 CC FET: M00737; HISTONE_H2B.
 CC SMART: SM00427; H2B, 1.
 CC PROSITE: PS00167; HISTONE_H2B, 1.
 CC NCBI: F00016; Chromosomal protein, nuclear, H2B family.
 CC Maltipase family.
 SQ SEQUENCE 150 AA; 15841 MW; 56AC2D527A6F5940 CRC64;

Query V11-A: 60 AA, Score 51, E-Val: 1e-107, 157;
 Best Local Similarity: 69.00, Ident: 60, Mismatches: 40, Indels: 0, Gaps: 0;
 Matches: 97, Conservative: 17, Mismatches: 40, Indels: 0, Gaps: 0;

QY 3 DGPYKPKKPKKSKK 15

||||| ||||| |||||

DE 30 DGPYKPKKPKKSKK 41

RESULT 3

YOUNG-TABE STANFORD, FET, 144 AA
 AC Q09261;
 DT 01-NOV-1997 (Pel 16, last sequence update)
 DT 01-NOV-1997 (Pel 16, last sequence update)
 DT 01-NOV-1997 (Pel 16, last sequence update)
 DE Hypothetical protein YOUNG-TABE, 144 AA.
 CS YOUNG-TABE, 144 AA.
 CC Caenorhabditis elegans.

CC Eukaryota; Metazoa; Embodiment; Eukaryota; Embodiment; Caenorhabditis;
 CC Phabidae; Phabidae; Caenorhabditis;
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC SPAIN-Bristol N2;
 RA Thomas K;
 RL Submitted (FEB-1995) to the EMBL/GenBank/DBJ databases.

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 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement. (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@sib-sib.ch).

CC EMBL: Y45244; CAAR0085.1;
 CC Wormpep: C32A3.2; CE01506.
 KW Hypothetical protein;
 SQ SEQUENCE 146 AA; 39221 MW; D511225F5042B420 CRC64;

Query March: 60 AA, Score 40, DB 1, Length 146;
 Best Local Similarity: 60.00, Ident: 60, Mismatches: 40, Indels: 0, Gaps: 0;
 Matches: 97, Conservative: 17, Mismatches: 40, Indels: 0, Gaps: 0;

QY 1 DGPYKPKKPKKSKK 15
 ||||| ||||| |||||
 DE 4 DGPYKPKKPKKSKK 18

RESULT 4

SRP14_MOUSE STANFORD, FET, 110 AA.
 AC P36354;
 DT 01-NOV-1990 (Pel 15, last sequence update)
 DT 01-NOV-1990 (Pel 15, last sequence update)
 DT 15-DEC-1998 (Pel 37, last annotation update)
 DE SRP14: 110 AA.
 GN SRP14.

OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Rodentia; Muridae; Muridae; Mus.
 CC Mammalia; Eutheria; Rodentia; Muridae; Muridae; Muridae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]

RP SEQUENCE FROM N.A. AND SEQUENCE OF 110 AND 77-95.
 RC MEHLING, J., Walter, P.,
 RA Strub, P., Walter, P.,
 PT "Isolation of a cDNA clone of the 14 kDa subunit of the signal
 PT recognition particle by direct hybridization of differentially primed
 PT polymerase chain reactions."

PL FET: M00737; HISTONE_H2B, 1.
 CC Maltipase family.
 RN [2]

PP X-RAY CRYSTALLOGRAPHY (2.53 ANGSTROMS).
 CC Maltipase family.
 FA FET: M00737; HISTONE_H2B, 1.
 PT "The crystal structure of the signal recognition particle Alu RNA
 PT binding heterodimer, SRP9/14."

RL EMBL: J. 16:3757-3766 (1997).
 CC -1- FUNCTION: SIGNAL RECOGNITION PARTICLE ASSEMBLY HAS A CRUCIAL ROLE
 CC IN TARGETING SECRETORY PROTEINS TO THE ER FOR TRANSLATION INTO THE
 CC MEMBRANE. SRP9 TOGETHER WITH SRP14 AND THE ALU PORTION OF THE SRP
 CC PNA, CONSTITUTES THE ELONGATION ASSEMBLY OF SRP. THE COMPLEX
 CC OF SRP9 AND SRP14 IS PROVIDED FOR SRP PNA BINDING.

CC -1- SUBUNIT: SIGNAL RECOGNITION PARTICLE CONSISTS OF A 70 KDA MOLECULE
 CC OF 14 KDA SUBUNIT AND SIX PROTEIN SUBUNITS: SRP9, SRP9C, SRP9D,
 CC SRP19, SRP14 AND SRP9.

CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- SIMILARITY: BELONGS TO THE SRP14 FAMILY.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL Data Bank.
 CC the European Bioinformatics Institute. There are no restrictions on its

Best local similarity 56.2%, Fred B. 21.
Matches 9; Conservative 1; Mismatches 6; Indels 4; Gaps 0;

QV 1 DRYVVVVVSPSPSPV 16
|| ||||| ||
DB 516 DQAVVVVVSPSPSPV 531

RESULT 14
TOP-DROME
ID TOP-DROME CRAMFASO, EST, 503 AA.
AC P18475;
DT 21-JUL-1996 (Seq. 15, Created)
ET 21-JUL-1996 (Seq. 16, Last sequence update)
FF 15-JUN-1996 (Seq. 41, Last annotation update)
FE Tyrosine protein kinase receptor and precursor (EC 2.7.1.112)
GN TOP
OS Prosopha melanogaster (Fruit fly)
OC Eukaryota, Metazoa, Arthropoda, Mandibulata, Pancrustacea, Hexapoda,
Insecta, Phryganea, Neoptera, Endopterygota, Diptera, Brachycera,
Mycetophaga, Ephyridiida, Eristalini, Eristalini,
Xenotaxia 7357,
RN (1) Taxid 7357,
RP SEQUENCE FROM N.A.
FX MEDLINE 9414054; PubMed 940396;
RA Sprenger F., Stevens L.M., Nusslein-Volhard C.
RT "The Drosophila gene also encodes a putative receptor tyrosine
kinase".
RL Nature 338:478-483 (1989).
RN (2)
RP CHARACTERIZATION.
RX MEDLINE 9414054; PubMed 940396;
RA Sprenger F., Torricelli M.M., Morrison D.K.
RT "Biochemical analysis of tyrosine and D-tyr during Prosopha
embryogenesis: implications for terminal sugar transduction".
RL Mol. cell Biol. 13:1163-1172 (1993).
CC - FUNCTION: PREPARE RECEPTOR WITH TYROSINE-PROTEIN KINASE ACTIVITY
REQUIRED FOR DETERMINATION OF ANTERIOR AND POSTERIOR TERMINAL
STRUCTURES IN THE PROSPHILA EMBRYO. THE LIGAND OF TOPK SEEMS TO
BE TSL.
CC - CATALYTIC ACTIVITY: ATP + a protein tyrosine + ADP + protein
tyrosine phosphate.
CC - SUBCELLULAR LOCATION: Type I membrane protein.
CC - TISSUE SPECIFICITY: EXPRESSED THROUGHOUT THE EMBRYO BUT IS
ACTIVATED SPECIFICALLY AT THE POLES.
CC - SIMILARITY: BELONGS TO THE TYP FAMILY OF PROTEIN KINASES.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL Outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (see <http://www.isb.ac.uk/embout/>)
or send an email to license@isb.ac.uk.

EMBL; X15157; CAA32247.1;
DB PIR; S03900; S03900
DB HSSP; P11362; IFSK
DB PIRBASE; PR0000719; Tyr
DB InterPro; IPR0000719; Euk_kinase.
DB InterPro; IPR001245; Ty_kinase.
DB Pfam; PF00072; Kinase.
DB Pfam; PF00001; Euk_kinase.
DB SMART; SM00119; Tyro1.
DR PROSITE; PS00167; PROTEIN_KINASE_ATP_1
DR PROSITE; PS00168; PROTEIN_KINASE_TYR_1
DR PROSITE; PS00111; PROTEIN_KINASE_TYR_1
KW Developmental protein; precursor; glycoprotein;
KW Tyrosine protein kinase; Ant binding; Transferrin; Phosphorylation;
KW Transmembrane; Signal.
FT SIGNAL 1 20 POTENTIAL
FT CHAIN 21 531 TYROSINE PROTEIN KINASE FF WITH 16KDa
FT DOMAIN 21 309 EXTRACELLULAR (POTENTIAL)

QV 1 DRYVVVVVSPSPSPV 16
|| ||||| ||
DB 516 DQAVVVVVSPSPSPV 531

RESULT 15
HI-PARAN
ID HI-PARAN STANDARD, EST, 248 AA.
AC P02256;
DT 21-JUL-1996 (Seq. 91, Created)
ET 21-JUL-1996 (Seq. 92, Last sequence update)
FF 15-JUN-1996 (Seq. 48, Last annotation update)
FE Histone H1, gonadal.
OS Parachinus aguilus (Angulate sea urchin)
OC Eukaryota, Metazoa, Echinodermata, Echinozoa, Echinozoa,
Echinodermata, Echinodermata, Echinodermata, Echinodermata,
Echinodermata, Echinodermata, Echinodermata, Echinodermata,
OC Parachinus.
CC NCHI_Taxid=7459;
RN (1)
PP SEQUENCE OF 1-84.
PP MEDLINE 9414054; PubMed 940396;
RA Suckland W.N., Suckland M., de Groot B.J., van Holt G.,
RA Wittmann-Liebold B.
RT "The primary structure of histone H1 from sperm of the sea urchin
Parachinus aguilus. 1. Chemical and enzymatic fragmentation of the
protein and the sequence of amino acids in the four N-terminal
cysteine-histidine peptides".
RL Eur. J. Biochem. 194:553-565 (1990).
RN (2)
FF SEQUENCE OF 80-248.
FX MEDLINE 9414054; PubMed 940396;
RA Suckland W.N., Suckland M., de Groot B.J., van Holt G.,
RA Wittmann-Liebold B.
RT "The primary structure of histone H1 from sperm of the sea urchin
Parachinus aguilus. 2. Sequence of the C-terminal cysteine and
the entire primary structure".
RL Eur. J. Biochem. 194:567-578 (1990).
CC FUNCTION: HISTONE H1: AFF NECESSARY FOR THE CONDENSATION OF
NUCLEOSOME "BRINGS INTO HIGH ORDER STRUCTURES".
CC - TISSUE SPECIFICITY: SPPM
CC - SIMILARITY: BELONGS TO THE HISTONE H1/F1 FAMILY.
DR HSSP; P02259; HIST.
DR InterPro; IPR001246; Histone_H1/H1F.
DR Pfam; PF00538; linker_histone_1.
DR Pfam; PF00537; linker_histone_1.
DR SMART; SM00116; H1s_1.





...peptides, particularly antimicrobial resistant
...are also useful as wound treatment agents to
...cell to matrix proteins, especially fibronectin,
...and for prophylaxis use in dental treatment as
...in conjunction with, antibiotic prophylaxis. (i)
...bacterial membranes which have a higher
...spholipids than the eukaryotic organisms, also
...ion of membrane associated biosynthetic proteins,
...used antimicrobial activity upon derivatisation
...to treat the antibiotic resistant bacterial
...AA122 represent peptides given in the
...treatment invention

Query Match 100.0%; Score 82; EB 19; Length 16;
Best Local Similarity 100.0%; Pred. No. 1, 6e-06;
Matches 16; Conservative 0; Mismatches 0; Gaps 0;

14; 17 AA;

Key Location/Qualifiers
Modified-site 17
/note: "myristoylated"

Key Location/Qualifiers
Modified-site 17
/note: "myristoylated"

Smith RAG, Bright JR, Steward M, Cox VF;
WPI; 2000-182406/16.

Smith RAG;

polypeptide's, inhibit low affinity
...useful for treating complement-related and
...involving improved inhibition at cellular

Smith;

...these represent a significantly claimed membrane
...invention relates to a peptide derivative (A) of a
...which comprises at least a hetero loop is
...the (MBE) of low membrane affinity equivalent
...MBE interact independently and with thermodynamic
...vents of cellular or artificial membranes expressed
...are used to treat disorders treatable with
...tly inflammation or any other complement-related
...disease, graft rejection, myocardial
...cardiac arthritis and many others; including
...in devices and therapeutic disease, but also to
...weight loss, to treat asthma or asthma and as
...taining multiple sclerosis. A are administered

CC orally, topically, by injection or inhalation at 0.1 to 10 preferably
CC 0.1-10 mg/kg/day.

SQ Sequence 17 AA;

Query Match 100.0%; Score 82; EB 19; Length 16;
Best Local Similarity 100.0%; Pred. No. 1, 6e-06;
Matches 16; Conservative 0; Mismatches 0; Gaps 0;

QY 1 DGPYRYYRYSK 16
|||||
DY 2 DGPYRYYRYSK 17

RESULT 5

AAV58864

ID AAV58864 standard; Peptide; 17 AA.

XX AC AAV58864;

XX DT 08-MAY-2000 (first entry)

XX DE Membrane binding element used in anti-angiogenic polypeptide.

XX KW Anti-angiogenic, angiogenesis inhibitor; membrane binding element;

XX OS Synthetic.

EH Key Location/Qualifiers

FT Modified-site 17

PT /note: "myristoylated"

PN W06000452.A2.

PD 27-JAN-2000.

PF 16-JUL-1999; 99WO-GR02292.

PR 16-JUL-1999; 99SR-0015505.

XX PA (ADPR-) ADPROTECH PLC.

XX PI Smith RAG, Bright JR, Steward M, Cox VF;

XX DR WPI; 2000-182406/16.

XX New soluble derivative of anti-angiogenic polypeptide useful for
treatment of primary or secondary cancers, contains covalently attached
membrane-binding elements for targeting .
PS Disclosure; Page 13; 36pp, English.

XX The present sequence is an example of a lysine-rich peptide
membrane binding element (MBE) that can be utilised in novel
soluble derivatives of anti-angiogenic polypeptides of the
invention. (i) comprise 2 or more heterocyclic MBEs with low
membrane affinity that are covalently attached to a soluble
anti-angiogenic polypeptide such as a non-catalytic region of human
plasminogen, fragments of related proteins containing kringle
domains, fragments of collagen or fibrinogen, neutralising
antibodies against receptors for angiogenic mediators, and
antagonists of integrins involved in cell adhesion. The MBEs
interact independently with their ligands. (ii) provide targeted
components of the vascular endothelium. (i) provide targeted
delivery of the anti-angiogenic polypeptide to cell surfaces and
sites of active angiogenesis, particularly the vascular endothelium,
and therefore increase the local concentration and reduce the risk
of adverse effects on normal processes elsewhere in the vasculature.
They are used in a claimed method of treatment of primary or
secondary tumour.

SQ Sequence 17 AA;

Query Match 100.0% Score 82; DB 21; Length 17;
 Best Local Similarity 100.0%; Pval N/A; Mismatches 0; Indels 0; Gaps 0;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PDPKPKPKPKPKPKPKSK 15
 |||||
 DB ? PDPKPKPKPKPKPKSK 17

RESULT 6

AAW45878
 ID AAW45878 standard; peptide; 16 AA.

XX AC AAW45878;

XX DT 30-JUN-1998 (first entry)

XX DE Peptide membrane binding element.

XX KW Membrane binding element; thrombotic disease; inflammation;
 XX PW complement related disease; soluble peptide

XX OS Synthetic

XX PN WCGR02474-A2

XX PD 22 JAN 1998.

XX PF 08 JUL 1997; QWO EP04716

XX PR 15 JUL 1996; GPCR-0014871

XX PA (ADPR-) AOPROTECH PLC.

XX PI Dodd I, Mossakowska DFI, Smith PAC;

XX DP WFI, 1998 110247/10

XX PT Derivatives of soluble fully peptide(s) bound to low affinity
 XX PT membrane binding groups useful for treating complement-related and
 XX PT thrombotic diseases, providing improved localisation at cellular
 XX PT membranes

XX PS Claim 11; Page 20; 25pp; English.

XX CC The present peptide sequence represents a specifically defined membrane
 CC binding element. The invention relates to a soluble derivative (A) of a
 CC soluble polypeptide (1), which comprises at least 2 heterologous
 CC membrane-binding elements (MBEs) of low membrane affinity associated
 CC associated with (1). MBE interact, independently and with thermodynamic
 CC additivity, with components of cellular or artificial membranes exposed
 CC to extracellular fluids. (A) are used to treat disorders treatable with
 CC (1) itself, specifically inflammation or any other complement-related
 CC disorder, e.g. neurological disease, graft rejection, myocardial
 CC infarction, sepsis, rheumatoid arthritis and many others; including
 CC application to indwelling devices) and thrombolytic disease, but also to
 CC treat allergy, induce weight loss, to treat ischemia or asthma and as
 CC immunomodulators for treating multiple sclerosis (A) are administered
 CC orally, intrally, by injection or inhalation at 0.01-10 (preferably
 CC 0.1-10) mg/kg/day

XX SQ Sequence 16 AA;

Query Match 93.0%; Score 77; DB 19; Length 16;

Best Local Similarity 100.0%; Pval N/A; Mismatches 0; Indels 0; Gaps 0;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PDPKPKPKPKPKPKSK 15

DB 1 PDPKPKPKPKPKPKSK 15

RESULT 7

AAV58855

ID AAV58855 standard; Peptide; 16 AA.

XX AC AAV58855;

XX DT 08-MAY-2000 (first entry)

XX DE Membrane binding element used in anti-angiogenic polypeptide.

XX PW Anti-angiogenic, angiogenesis inhibitor, membrane binding element;
 XX KW cancer; tumour; therapy.

XX OS Synthetic.

XX PN WO200004052-A2.

XX PD 27-JAN-2000.

XX PF 16 JUL 1999; 99WO GB02292.

XX PP 16-JUL-1999; GPCR-0014505.

XX PA (ADPR-) ADPROTECH PLC.

XX PI Smith PAC, Bright JR, Steward M, Cox VF;

XX DP WFI, 2000 102406/16.

XX PT New soluble derivative of anti-angiogenic polypeptide useful for
 XX PT treatment of primary or secondary cancers, contains covalently attached
 XX PT membrane-binding elements for targeting

XX PS Claim 14; Page 34; 35pp; English.

XX CC The present sequence is a claimed example of a lysine-rich peptide
 CC membrane binding element (MBE) that can be utilized to target
 CC soluble derivatives (A) of anti-angiogenic polypeptides to the
 CC intervention. (A) comprise 2 or more heterologous MBEs with low
 CC membrane affinity that are covalently attached to a soluble
 CC anti-angiogenic polypeptide (1) and a third region of human
 CC plasmaogen, fragments of related proteins containing kringle
 CC domains, fragments of collagen or prolactin, neutralising
 CC antibodies against receptors for angiogenic mediators, and
 CC antagonists of integrins involved in angiogenesis. The MBEs
 CC interact independently with thermodynamic additivity, with
 CC each other and the vascular endothelium. (A) provide targeted
 CC delivery of the anti-angiogenic polypeptide to cell membranes and
 CC sites of active angiogenesis, particularly the vascular endothelium,
 CC and therefore increase the local concentration and efficacy of the
 CC of adverse effects on normal processes elsewhere in the vasculature.
 CC They are used in a clinical method for treatment of primary or
 CC secondary tumour.

XX SQ Sequence 16 AA;

Query Match 93.0%; Score 77; DB 21; Length 16;

Best Local Similarity 100.0%; Pval N/A; Mismatches 0; Indels 0; Gaps 0;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PDPKPKPKPKPKPKSK 15

DB 1 PDPKPKPKPKPKPKSK 15

RESULT 8

ABB91237

ID ABB91237 standard; peptide; 16 AA.

XX AC ABB91237;

XX DT 20-AUG-2002 (first entry)

XX XX

RESULT 14

AAW45898
 ID AAW45898 standard; peptide; 214 AA.
 XX
 AC AAW45898;
 XX
 DT 10-JUN-1999 (first entry)
 XX
 DE SCR 1-3 of complement receptor type 1 (CR1)/switch fusion protein.
 XX
 FE Membrane binding element, therapeutic disease, soluble protein.
 XX
 FE Complement-related disease, integral membrane protein, inflammation.
 XX
 FE Short consensus repeat; SCR 1, C1q, complement receptor type 1.
 XX
 CC Homo sapiens.
 XX
 FE Key Location/Qualifiers
 FE Cross-links 214
 FE /note- "Disulphide linked to Cys in peptide given
 FE in AAW45898 or 2 (CHL2209H(CHL2120H3".
 FT
 FT W09AC2454 A2.
 PN
 XX 22 JAN-1999.
 XX
 XX 08-JUL-1997; 97WO-EP03715.
 XX
 XX 15-JUL-1996; 96GB-0014871.
 PR
 XX (ADPR-) ADPROTECH PLC.
 PA
 XX Dredd I, Massakowska DEL, Smith PAG;
 PI
 XX WPI; 1998-110524/10.
 DR
 XX
 XX Derivatives of soluble glycopeptide(s) tended to low affinity
 PT membrane binding groups - useful for treating complement-related and
 PT thrombotic diseases, providing improved localisation at cellular
 PT membranes
 XX
 XX Claim 22, Page 62, Tiff, English
 PS
 XX This sequence represents a specifically claimed protein having the
 XX amino acid sequence of short consensus repeats (SCR 1-3) of
 CC complement receptor type (CRP) plus a switch fusion sequence. The
 CC fusion is related to a soluble derivative (A) of a soluble polypeptide
 CC (1), which comprises at least 2 heterologous membrane-binding elements
 CC (MRPs) of low membrane affinity covalently associated with (ii) MRP
 CC interact, independently and with thermodynamic additivity, with
 CC components of cellular or artificial membranes exposed to extracellular
 CC fluids. (A) are used to treat disorders treatable with (ii) itself,
 CC or 3 therapeutic diseases, graft rejection, myocardial infarction,
 CC sepsis, rheumatoid arthritis and many others, including application to
 CC indwelling devices) and thrombolytic disease, but also to treat allergy,
 CC induce weight loss, to treat ischaemia or asthma and as immunosuppressants
 CC for treating multiple sclerosis. (A) are administered orally,
 CC topically, by injection or inhalation and/or by preferential local
 CC administration.
 XX
 XX Sequence 214 AA;
 SQ
 Query March 01 04; Query 75, 78 191, length 214.
 Best local similarity: 100.00, 200.00, 200.00
 Matches: 10, Conservation: 10, Mismatches: 0, Indels: 0, Gaps: 0,
 QY 1 DTTTTTTTTTTTSPSS 15
 DB 198 DTTTTTTTTTTTSPSS 210

RESULT 15

AAW75987
 ID AAW75987 standard; Protein; 215 AA.
 XX
 AC AAW75987;
 XX
 DT 18-JAN-1999 (first entry)
 XX
 DE Complement receptor type 1-like polypeptide (PM-9).
 XX
 FE Complement receptor type-1; C1q, C1q, PM-9, complement, inhibitor;
 FE myristoyl/electrostatic switch peptide reagent 1; MSWP-1;
 FE anti-fibrinolytic; multiple solid; PM, Parkinson's disease;
 FE xenograft rejection, inflammation, Crohn's disease, asthma;
 FE paracetamol, first ischaemic reperfusion, infection, sepsis;
 FE autoimmune disease; rheumatoid arthritis; proliferative nephritis;
 FE myasthenia gravis; reproductive disorder; therapy.
 XX
 OS Chimeric - Homo sapiens.
 OS Chimeric - Synthetic.
 XX
 FE Key Location/Qualifiers
 FE Protein 1..197
 FE /label= CW7
 FE Peptide 199..215
 FE /label= MSWP-1
 FE Disulfide-bond 199..199
 FE Modified-site 199
 FE Modified-site /note= "(S-2 thiopyridyl)cysteine"
 FT 215
 FT /note= "N (myristoyl) Glycine"
 XX
 XX W09839433-A1.
 PN
 XX 11-SEP-1998.
 PD
 XX 05-MAR-1998; 98WO-GB00727.
 PF
 XX 05-MAR-1997; 97GB-0004719.
 PF
 XX (ADPR-) ADPROTECH PLC.
 PA
 XX Cox VP, Massakowska DEL, Smith PAG;
 PI
 XX WPI; 1998-0004719.
 DR
 XX Soluble polypeptide comprising short consensus repeats from LRR A
 PT used to treat disorders and diseases associated with inflammation or
 PT inappropriate complement activation
 XX
 XX Claim 17, Page 50-52, 67ff, English.
 PS
 XX This is the amino acid sequence of PM 1, a novel Cys-D-S (MSWP-1),
 XX comprising novel soluble complement receptor type 1 (C1q) like
 XX polypeptide (PM) (see AAW75987) joined to a myristoyl/electrostatic
 XX switch peptide reagent 1 (MSWP-1). It was prepared by coupling
 XX CMT/Cys (see AAW75987) to a synthetic MSWP-1 peptide. CMT comprises
 XX the short consensus repeats (SCR) 1 and 2 from C1q and SCR of the
 XX C1q-like protein (see AAW75987). Soluble C1q derived proteins of the
 XX invention (see AAW75987) and AAW75987 act as complement inhibitors
 XX with functional complement inhibitory, including anti-hemolytic,
 XX activity. These can be used to treat a disease or disorder
 XX associated with inflammation or inappropriate complement activation,
 XX such as neurological disorders (eg, multiple sclerosis, Parkinson's
 XX disease), disorders of inflammation or infection (eg, complement
 XX activation, disorders of inflammation or infection, inflammatory disorders (eg,
 XX rheumatoid disease, asthma, and acute promyelocytic leukaemia),
 XX reperfusion syndromes, infection, sepsis, myocardial infarction,
 XX disorders and autoimmune disease (eg, rheumatoid arthritis,
 XX proliferative nephritis and myasthenia gravis), and reproductive
 XX disorders
 XX
 XX Sequence 215 AA;
 SQ

41, Score 77; IP 10, end 215;
20; Pred. No. 111;
; Mismatches 0; Indels 0; Gaps 0;

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MACROMOLECULE DELIVERY

NUMBER OF SEQUENCES: 199
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Lyon & Lyon
 STREET: 444 West Fifth Street
 SUITE: 4700
 CITY: Los Angeles
 STATE: California
 COUNTRY: U.S.A.
 ZIP: 90071-2016
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

COMPUTER: IBM compatible
 OPERATING SYSTEM: IBM PC DOS 6.0
 SOFTWARE: Word Perfect 6.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/806,401

FILING DATE: 12-Mar-2001

CLASSIFICATION: unknown

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/84,342

FILING DATE: unknown

ATTORNEY/AGENT INFORMATION:

NAME: Warburg, Richard J.

REGISTRATION NUMBER: 30,327

PREFERENCE/COCKET NUMBER: 21/180

TELECOMMUNICATION INFORMATION:

TELEPHONE: 213/494-1700

TELEFAX: 213/494-0440

TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 78:

SEQUENCE CHARACTERISTICS:

LENGTH: 17 amino acids

TYPE: amino acid

SPERMATIN: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 78:

US 09 806 401 78

Query Match: 59.51% Score 47, DB 10, Length 17,

Best Local Similarity: 57.18% Pred. No. 11;

Matches: 8; Conservative: 3; Mismatches: 4; Indels: 1; Gaps: 0;

US 09 806 401 78

US 09 806 401 78

US 09 806 401 78

US 09 806 401 78

US 09 806 401 78

US 09 806 401 78

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US 09 806 401 78

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US 09 806 401 78

US 09 806 401 78


```

/ NAME/KEY SITE
/ LOCATION: (96)
/ OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
/ NAME/KEY SITE
/ LOCATION: (128)
/ OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
/ NAME/KEY SITE
/ LOCATION: (147)
/ OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US 00 764 864 1299

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Query Match	56.13	Score 46	DB 10	Length 147
Best Local Similarity	56.04	Prod No 10		
Matches	9	Conservative	0	Mismatches 7
				Indels 0
				Gaps 0

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RESULT 9
US-04-49,000,000,1947
; Sequence 1047, Application US/04042949
; Patent No. US040405527A1
; GENERAL INFORMATION
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: P402
; CURRENT APPLICATION NUMBER: US/04/045,000
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05843
; PRIOR FILING DATE: 2000-04-08
; PRIOR APPLICATION NUMBER: 40/134,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1556
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1087
; LENGTH: 154

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APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA102
CURRENT APPLICATION NUMBER: US/23/225,299
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05883
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 50/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1556
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1408
LENGTH: 36
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (4)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (6)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (8)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (12)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (13)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (36)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-299-1408

Query Match 54.9%; Score 45; DB 10; Length 36;
Best local similarity 60.9%, Pred. No. 3.9,
Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

CY 2 GPPKFKKSPKSK 16
| | | | | | | | | |
DB 20 GPPKFKKSPKSK 34

Search completed Mon Mar 3, 2003, at 11:33
Job time: 48.0244 secs

Text in version 9.1.1. Copyright © 1993 - 2003. All rights reserved.

$$z_{\text{new}} = \text{model}(x_{\text{new}})$$

. . . 0:23 : Start time : 1973 seconds
 (WLFreq = 60 Hertz)
 46.78 Hz @ 0.011 updates/sec

1

1. *Introduction*
 2. *Method*
 3. *Results*
 4. *Discussion*
 5. *Conclusion*
 6. *References*
 7. *Appendix*
 8. *Notes*
 9. *Tables*
 10. *Figures*
 11. *Supplementary Materials*
 12. *References*
 13. *Appendix*
 14. *Notes*
 15. *Tables*
 16. *Figures*
 17. *Supplementary Materials*
 18. *References*
 19. *Appendix*
 20. *Notes*
 21. *Tables*
 22. *Figures*
 23. *Supplementary Materials*
 24. *References*
 25. *Appendix*
 26. *Notes*
 27. *Tables*
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2014. 4. 10

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W. J. P. / H. J. P.

[illegible]

of results predicted by them to have a
equal to the score of the result being printed,
size of the total score was calculated.

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Db 516 DGPYKPKKSKSK 531

RESULT 6

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 1 Sequence 6, Application US-09-2114-913-40-rai
 2 Patent No. 5705334
 3 GENERAL INFORMATION
 4 APPLICANT: Lippard, Stephen J.
 5 APPLICANT: Essigmann, John M.
 6 APPLICANT: Donahue, Brian A.
 7 APPLICANT: Toney, Jeffrey H.
 8 APPLICANT: Bruhn, Suzanne L.
 9 APPLICANT: Pili, Pieter M.

US-09-2114-913-40-rai

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US-09-2114-913-40-rai

APPLICANT: Brown, Steven
APPLICANT: Kellott, Patti
TITLE OF INVENTION: Uses For DNA Structure Specific
TITLE OF INVENTION: Recognition Proteins
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patent Administration, Testa, Hurwitz & Thibault
STREET: 53 State Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/125,409
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Fenton, Gillian M
REGISTRATION NUMBER: 36,508
REFERENCE/AGENT INFORMATION: MIT 617-253-1110
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-248-7000
TELEFAX: 617-248-7100
INFORMATION FOR SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
LENGTH: 723 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Drosophila melanogaster
IMMEDIATE SOURCE:
CLONE: Drosophila SSGP (predicted)
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LOCATION: 547-620
OTHER INFORMATION: /label= Mixed Charge
US 08/125,409-6

Query Match 56.1% Date 05/28/03 Length 723

Best total similarity 56.1% Pos 231-237

No gaps 0, Conservative 1, Mismatches 6, Indels 0, Bfg

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0B 514 DDDDDDDDDDDDDDD 51

RESULT 7

PCT-US92 11107 11

Sequence 11: Application PCTUS-11107

GENERAL INFORMATION:

APPLICANT: Donahue, Brian A.
APPLICANT: Toney, Jeffrey H.
APPLICANT: Fruhn, Suzanne L.
APPLICANT: Pili, Pieter M.
APPLICANT: Brown, Steven
APPLICANT: Kellott, Patti
APPLICANT: Fessigmann, John M.
APPLICANT: Lippard, Stephen J.
TITLE OF INVENTION: DNA Structure Specific Recognition
TITLE OF INVENTION: Protein and Uses Therefor
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brock, Smith & Reynolds, P.C.
STREET: 2 Militia Drive
CITY: Lexington
STATE: MA
COUNTRY: USA
ZIP: 01173
COMPUTER READABLE FORM
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US 92/11107
FILING DATE: 19921218
CLASSIFICATION:
PCT APPLICATION DATA:
APPLICATION NUMBER: US 92/589,926
FILING DATE: 19 JUN 1990
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 23,227
REFERENCE/AGENT INFORMATION: MIT-4787AAA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
TELEFAX: 617-861-9540
INFORMATION FOR SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
LENGTH: 723 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Drosophila melanogaster
IMMEDIATE SOURCE:
CLONE: Drosophila SSGP (predicted)
FEATURE:
NAME/KEY: Domain
LOCATION: 458-507
OTHER INFORMATION: /label= Acidic
FEATURE:
NAME/KEY: Domain
LOCATION: 518-547
OTHER INFORMATION: /label= Basic I
FEATURE:
NAME/KEY: Domain
LOCATION: 547-620
OTHER INFORMATION: /label= Mixed Charge
FEATURE:
NAME/KEY: Domain
LOCATION: 657-723
OTHER INFORMATION: /label= Mixed Charge
PCT-US92-11107-11

Query Match

Best total similarity 56.1% Pos 231-237

Mismatches 6, Conservative 1, Mismatches 6, Indels 0, Bfg

Patent No. 6040140
GENERAL INFORMATION:
APPLICANT: Croce, Carlo
APPLICANT: Ganaani, Eli
TITLE OF INVENTION: Diagnostics, Therapeutics and Methods
for Detection and Treatment of Acute Leukemias
TITLE OF INVENTION: Resulting from Chromosome Abnormalities in the A11.1 Region
NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock, Washburn, Kuriz, Mackiewicz &
ADDRESS: No. 6040140ris
STREET: One Liberty Place, 46th floor
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
FORMAT: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/545,860D
FILING DATE: 07-MAR-1996
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/04496
FILING DATE: 22-APR-1994
PRIOR APPLICATION DATA: PCT/US92/10390
APPLICATION NUMBER: PCT/US92/10390
FILING DATE: 09-DEC-1992
PRIOR APPLICATION DATA: US 08/327,352
APPLICATION NUMBER: US 08/327,352
FILING DATE: 19-OCT-1994
PRIOR APPLICATION DATA: US 08/320,550
APPLICATION NUMBER: US 08/320,550
FILING DATE: 11-OCT-1994
PRIOR APPLICATION DATA: US 09/062,443
APPLICATION NUMBER: US 09/062,443
FILING DATE: 14-MAY-1993
PRIOR APPLICATION DATA: US 07/971,094
APPLICATION NUMBER: US 07/971,094
FILING DATE: 30-OCT-1992
PRIOR APPLICATION DATA: US 08/886,839
APPLICATION NUMBER: US 08/886,839
FILING DATE: 27-MAY-1992
PRIOR APPLICATION DATA: US 07/835,093
APPLICATION NUMBER: US 07/835,093
FILING DATE: 11-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Deluca Esq. Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TCU 1262
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 559 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-545-860D-31

Query Match: 55.5%; Score 45.57; DB 3; Length 559;
Best Local Similarity 57.9%; Pred. No. 27;
Matches 11; Conservative 2; Mismatches 3; Indels 3; Gaps 1;
QY 1 DDPF---PPPPPPPPPPPP 16
DE 231 DDPFSAFFPPPPPPPPPP 309

Diagnostics, Therapeutics and Methods for
Detection and Treatment of Acute Leukemias
Resulting from Chromosome Abnormalities in the
A11 Region
US-08-545-860D-31
Length: 559 amino acids
Type: amino acid
Strandedness: single
Topology: linear
Molecule type: protein
US-08-545-860D-31
Query Match: 55.5%; Score 45.57; DB 3; Length 559;
Best Local Similarity 57.9%; Pred. No. 27;
Matches 11; Conservative 2; Mismatches 3; Indels 3; Gaps 1;
QY 1 DDPF---PPPPPPPPPPPP 16
DE 231 DDPFSAFFPPPPPPPPPP 309

RESULT 10
PCT-US-94-04456-11
Sequence 5, Application US/09306044
GENERAL INFORMATION:
APPLICANT: GROCE, CARLO
APPLICANT: CANAANI, ERI
TITLE OF INVENTION: Diagnostic, Therapeutic and Methods
TITLE OF INVENTION: Detection and Treatment of Acute Leukemia
TITLE OF INVENTION: Resulting from Chromosome Abnormalities in the A11
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: Washburn, Washburn, Kurtz, Mack-Lewitz &
ADDRESSEE: Norris
STREET: One Liberty Place, 46th floor
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.02
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/04456
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: DeLuca Esq., Mark
REGISTRATION NUMBER: 31,229
REFERENCE/PATENT NUMBER: T39 1242
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568 3100
TELEFAX: (215) 568 3439
INFORMATION FOR SEQ ID NO. 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 559 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US-94-04456-11

Query Match 54.9%, Score 46.5, E-Value 1.0, Length 559,
Best Local Similarity 59.0%, Pct. No. 37,
Matches 11; Conservation 2, Mismatches 3, Indels 3, Gaps 1.

27 1 GRY PFFPKSPSPSSK 16
||| ||||| |||
Db 271 DEPRFAAPFSPSSPSSP 309

RESULT 11
US-09-214-913-40-5
Sequence 5, Application US/09306044
Patent No. 5945400
GENERAL INFORMATION:
APPLICANT: SHERMAN, DANIEL
APPLICANT: RYK, GERARDO
APPLICANT: SCHWARTZ, BERTRAND
TITLE OF INVENTION: NUCLEIC ACID CONTAINING COMPOSITION,
PREPARATION AND USE THEREOF
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pharm-Polysar, Peter Inc.
STREET: 500 Arcola Road, Mailstop 3043
CITY: Collegeville
STATE: PA
COUNTRY: USA
ZIP: 19426
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.10
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09306044
FILING DATE:
CLASSIFICATION: 514
PRIORITY APPLICATION DATA:
PRIORITY NUMBER: PCT/US94/00248
FILING DATE: 15-FEB-1996
PRIORITY APPLICATION DATA:
PRIORITY NUMBER: WO PCT/FR94/00248
FILING DATE: 15-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Cavitzky Esq., Martin F.
REGISTRATION NUMBER: 29,899
REFERENCE/PATENT NUMBER: T39 1242
TELECOMMUNICATION INFORMATION:
TELEPHONE: (610) 454-3816
TELEFAX: (610) 454-3808
INFORMATION FOR SEQ ID NO. 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-894-339-5

Query Match 54.9%, Score 45, E-Value 1.0, Length 17,
Best Local Similarity 59.0%, Pct. No. 11,
Matches 8; Conservation 2, Mismatches 4, Indels 0, Gaps 0.

27 3 PFFPKSPSPSSK 16
||| ||||| |||
271 DEPRFAAPFSPSSPSSP 16

RESULT 12
US-09-306-044-5
Sequence 5, Application US/09306044
Patent No. 5945400
GENERAL INFORMATION:
APPLICANT: SHERMAN, DANIEL
APPLICANT: RYK, GERARDO
APPLICANT: SCHWARTZ, BERTRAND
TITLE OF INVENTION: NUCLEIC ACID CONTAINING COMPOSITION,
PREPARATION AND USE THEREOF
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pharm-Polysar, Peter Inc.
STREET: 500 Arcola Road, Mailstop 3043
CITY: Collegeville
STATE: PA
COUNTRY: USA
ZIP: 19426
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09306044
FILING DATE:
CLASSIFICATION:
PRIORITY APPLICATION DATA:
PRIORITY NUMBER: PCT/US94/00248
FILING DATE: 15-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Cavitzky Esq., Martin F.

Best Local Similarity 57.1%; Pred. No. 13;
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
CY 3 PPKYKSPKSK 16
DB 146 PPKSAKTPPKAK 159
RESULT 14
US-08-837-058-1
; Sequence 1, Application US/08837058
; Patent No. 6074835
; GENERAL INFORMATION:
; APPLICANT: Braun, Jonathan
; APPLICANT: Targan, Stephan R.
; APPLICANT: Eggena, Mark
; TITLE OF INVENTION: Diagnosis, Prevention and Treatment of
; TITLE OF INVENTION: Ulcerative Colitis, and Clinical Subtypes Thereof, "B-1"
; TITLE OF INVENTION: Histone H1
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 300
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; CREATING SYSTEM: PC-EMMS-UCS
; SOFTWARE: Patent Release #1.0, Version #1.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/837,158
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-PK 2419
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 212 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1-212
; OTHER INFORMATION: /note="product - Human Histone
; OTHER INFORMATION: H1-S-1"
US-08-837-058-1
Query Match 54.9%; Score 45; DB 3; Length 212;
Best Local Similarity 57.1%; Pred. No. 13;
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
CY 3 PPKYKSPKSK 16
DB 146 PPKSAKTPPKAK 159
RESULT 15
US-09-041-889-4
; Sequence 4, Application US/09041889
; Patent No. 6033864
; GENERAL INFORMATION:
; APPLICANT: Braun, Jonathan
; APPLICANT: Coravy, Ofer
; TITLE OF INVENTION: Diagnosis, Prevention and Treatment of
; TITLE OF INVENTION: Ulcerative Colitis, and Clinical Subtypes Thereof, "B-1"

21,609
US-09-041-889-4
; Sequence 4, Application US/09041889
; Patent No. 6033864
; GENERAL INFORMATION:
; APPLICANT: Braun, Jonathan
; APPLICANT: Coravy, Ofer
; TITLE OF INVENTION: Diagnosis, Prevention and Treatment of
; TITLE OF INVENTION: Ulcerative Colitis, and Clinical Subtypes Thereof, "B-1"
; TITLE OF INVENTION: Histone H1
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 300
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; CREATING SYSTEM: PC-EMMS-UCS
; SOFTWARE: Patent Release #1.0, Version #1.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/041,889
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-PK 2419
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 212 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1-212
; OTHER INFORMATION: /note="product - Human Histone
; OTHER INFORMATION: H1-S-1"
US-09-041-889-4
Query Match 54.9%; Score 45; DB 3; Length 212;
Best Local Similarity 57.1%; Pred. No. 13;
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
CY 3 PPKYKSPKSK 16
DB 146 PPKSAKTPPKAK 159
RESULT 15
US-09-041-889-4
; Sequence 4, Application US/09041889
; Patent No. 6033864
; GENERAL INFORMATION:
; APPLICANT: Braun, Jonathan
; APPLICANT: Coravy, Ofer
; TITLE OF INVENTION: Diagnosis, Prevention and Treatment of
; TITLE OF INVENTION: Ulcerative Colitis, and Clinical Subtypes Thereof, "B-1"

```

1 TITLE OF INVENTION: Microbial UC PANCA antigens
2 NUMBER OF SEQUENCES: 41
3 CORRESPONDENCE ADDRESS:
4 ADDRESSEE: Campbell & Flores LLP
5 STREET: 4370 La Jolla Village Drive, Suite 700
6 CITY: San Diego
7 STATE: California
8 COUNTRY: USA
9 ZIP: 92122
10 COMPUTER READABLE FORM:
11 MEDIUM TYPE: Floppy disk
12 COMPUTER: IBM PC Compatible
13 OPERATING SYSTEM: PC DOS/MS-DOS
14 SOFTWARE: PatentIn Release #1.0, Version #1.25
15 CURRENT APPLICATION DATA: /na/na41.raa
16 APPLICATION NUMBER: us/na/na41.raa
17 FILING DATE:
18 CLASSIFICATION:
19 PRIOR APPLICATION DATA:
20 APPLICATION NUMBER: US 08/837,058
21 FILING DATE: 11-APR-1997
22 ATTORNEY/AGENT INFORMATION:
23 NAME: Campbell, Cathryn A.
24 REGISTRATION NUMBER: 31,815
25 REFERENCE/DOCKET NUMBER: P-PM 3006
26 TELECOMMUNICATION INFORMATION:
27 TELEPHONE: (619) 535-9001
28 TELEFAX: (619) 535-8949
29 INFORMATION FOR SEQ ID NO: 4:
30 SEQUENCE CHARACTERISTICS:
31 LENGTH: 218 amino acids
32 TYPE: amino acid
33 TOPOLOGY: linear
34 FEATURE:
35 NAME/KEY: Peptide
36 LOCATION: 1..218
37 OTHER INFORMATION: /note="product = Human Histone
38 OTHER INFORMATION: H1-S-4"
39 US-09-041-889-4

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Query Match 54.9%; Score 45; DB 3; Length 218;

Best Local Similarity 57.1%; Pred. No. 13;

Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 3 PRRFFKSPGSK 16

DB 146 PRYSAXTPPKAK 159

Search completed: March 3, 2003, 06:15:50
Job time: 10.1463 secs

C:Accession: T46464

R:Ansoorge, W.; Winkner, U.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, January 2000

A:Reference number: 233028

A:Accession: T46464

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-542 <AAA>

A:Cross-references: EMBL:AL137421

A:Experimental source: skin, testis, 1 day TGF β 1449900

C:Genetics:

A:Note: DXP2434P072.1

Query Match 75.9% Score 51; DB 2; Length 542;

Best Local Similarity 71.4% Pred. No. 4.4;

Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

CY 1 SPGKPKPKPKPKPK 14

DB 245 SPGKPKPKPKPKPK 258

RESULT 9

C65608

Hypothetical protein T46464 (uniprot) Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse ear cross)

C:Date: 10 Mar 2001 #sequence_revision 02-Mar-2001 #text_change 1: Mismatch

C:Accession: C65608

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-522 <GTC>

A:Cross-references: JGI:AC003919, EMBL:AF019011, GenBank: AF019011

C:Genetics:

A:Gene: P25P12.91

A:Map position: 1

Query Match 74.1% Score 52; DB 2; Length 522;

Best Local Similarity 71.4% Pred. No. 4.4;

Matches 10; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

CY 1 SPGKPKPKPKPKPK 14

DB 424 SPGKPKPKPKPKPK 437

RESULT 10

JQ0129

86K heat shock protein IV - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 14 Sep 1998 #sequence_revision 04-Sep-1998 #text_change 14 Sep 1998

C:Accession: JQ0129

A>Status: preliminary

A:Molecule type: DNA, mRNA

A:Residues: 1-311 <WAL>

A:Cross-references: JGI:AC003919, EMBL:AF019011, GenBank: AF019011

C:Genetics:

A:Gene: P25P12.91

A:Map position: 1

Query Match 74.1% Score 52; DB 2; Length 522;

Best Local Similarity 71.4% Pred. No. 4.4;

Matches 10; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

CY 1 SPGKPKPKPKPKPK 14

DB 424 SPGKPKPKPKPKPK 437

Query Match 72.9% Score 51; DB 2; Length 511;

Best Local Similarity 76.9% Pred. No. 5.3;

Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

CY 2 KQKPKPKPKPKPK 14

DB 270 KQKPKPKPKPKPK 283

RESULT 11

A87913

Protein B0205.10 (imported) - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 10 May 2001 #sequence_revision 10-May-2001 #text_change 1: 10 May 2001

C:Accession: A87913

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-455 <STG>

A:Cross-references: JGI:AC003919, EMBL:AF019011, GenBank: AF019011

C:Genetics:

A:Gene: P25P12.91

A:Map position: 1

Query Match 72.9% Score 51; DB 2; Length 455;

Best Local Similarity 76.9% Pred. No. 5.3;

Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

CY 2 KQKPKPKPKPKPK 14

DB 423 KQKPKPKPKPKPK 443

RESULT 12

T06429

Hypothetical protein T06429 (uniprot) Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse ear cross)

C:Date: 06-Apr-1998 #sequence_revision 06-Apr-1998 #text_change 1: Aug 1998

C:Accession: T06429

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-756 <BEV>

A:Cross-references: JGI:AC003919, EMBL:AF019011, GenBank: AF019011

C:Genetics:

A:Gene: P25P12.91

A:Map position: 4

A:Introns: 494/1

A:Note: TSK18.240

Query Match 72.9% Score 51; DB 2; Length 756;

Best Local Similarity 83.3% Pred. No. 11;

Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

CY 2 KQKPKPKPKPKPK 14

DB 707 KQKPKPKPKPKPK 748

RESULT 13

C85220

Hypothetical protein AT4G10420 (imported) - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse ear cross)

C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 1: Feb-2001

in Arabidopsis Genome Sequencing Consortium, The Arabidopsis
Genome Initiative, 2000. Arabidopsis thaliana.
GeneID:2093488; PMID:119194

254; NID:97268741; PDB: 1Y4E.1; GSPDB:GN00140

48; Score 51; IP: 1000000000
48; Pred. No. 11; Mismatches 0; Indels 0; Gaps 0;

Genorhabdilis albus
Provision 15-Oct-1999

Entry, November 1999
f. elegans cosmid 1111.

Cloned from 35/EMBL 1999

32; PDB: ABE5387A.1; PDB: 1Y4E.1; GSPDB:GN00140
PDB: 1Y4E.1; GSPDB:GN00140

254 3; 16073; 1000000000

48; Score 50; IP: 1000000000
48; Pred. No. 11; Mismatches 0; Indels 0; Gaps 0;

1999 13-Aug-1999
1999 13-Aug-1999

1999 13-Aug-1999

1999 13-Aug-1999

1999 13-Aug-1999

48; PDB: 1Y4E.1; GSPDB:GN00140
48; PDB: 1Y4E.1; GSPDB:GN00140

48; Score 49; IP: 1000000000



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DR EMBL; X85754; CAA59755.1; --
DR HSSP; P01112; IPLL.
DR InterPro; IPR003577; GTPase pas.
DR InterPro; IPR001230; Prenyl site.
DR InterPro; IPR001806; Ras trnsfmg.
DR InterPro; IPR005225; Small GTP.
DR Pfam; PF00071; ras; 1.
DR PRINTS; PR00449; RASTRNSFRMNG.
DR SMART; SM00173; RAS; 1.
DR TIGRFAMs; TIGR00231; small GTP; 1.
ZW Pfam; Pfam00071; GTP-binding; Prenylation; Lipoprotein.
FT NP_BIND 10 17 GTP (BY SIMILARITY).
FT NP_BIND 57 61 GTP (BY SIMILARITY).
FT NP_BIND 116 119 GTP (BY SIMILARITY).
FT DOMAIN 32 40 EFFECTOR REGION (BY SIMILARITY).
FT LIPID 185 185 FARNESYL (BY SIMILARITY).
SQ SEQUENCE 188 AA; 21452 MW; AAB6C198B259865 CR64;

Query Match: 95.7%; Score 67; GI: Length 188
Best local similarity: 92.1%; Field No. 00044;
Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SPEDXXXXXXXXXX 14
DB 171 SEDGXXXXXXXXXX 184

RESULT 4
PASK_CYPCA STANDARD; PRT; 188 AA.
AC Q9YH38; 2000 (rel. 39, Created:
DT 30-MAY-2000 (rel. 39, Last sequence update:
DT 16-OCT-2001 (rel. 40, Last annotation update:
DE Transforming protein p21 (K-Ras) (K1-Pas).
GN KRAS.
OS Cyprinus carpio (Common carp).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Cyprinus.
OX NCBI_TaxID-7962;
RN [1]
RP SEQUENCE FROM N.A.
RA Chang M S, Chang Y, Chang G D, Huang F H, Hwang H J,
PT "Molecular cloning and sequencing of two carp cDNAs encoding ras
PT related proteins."
PI submitted (Appended to the EMBL/GenBank/DBP databases)
TI FUNCTION: RAS (RAS) IS A GTP-BINDING PROTEIN THAT
CC ACTIVITY.
CC -- PRTYPE REGULATION: ALTERNATE BETWEEN AN INACTIVE FORM BOUND TO GDP
CC AND AN ACTIVE FORM BOUND TO GTP. ACTIVATED BY A KINASE
CC NUCLEOTIDE-EXCHANGE FACTOR (GEF) AND INACTIVATED BY A PHASE-
CC ACTIVATING PROTEIN (GAP).
CC -- SIMILARITY: BELONGS TO THE SMALL GTPASE SUPERFAMILY. RAS FAMILY.
CC
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CC or send an email to license@sib-sib.ch).

DR EMBL; U53782; AAC05839.1; --
DR HSSP; P01112; IPLL.

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CC or send an email to license@sib-sib.ch).

DR EMBL; X85754; CAA59755.1; --
DR HSSP; P01112; IPLL.
DR InterPro; IPR003577; GTPase pas.
DR InterPro; IPR001230; Prenyl site.
DR InterPro; IPR001806; Ras trnsfmg.
DR InterPro; IPR005225; Small GTP.
DR Pfam; PF00071; ras; 1.
DR PRINTS; PR00449; RASTRNSFRMNG.
DR SMART; SM00173; RAS; 1.
DR TIGRFAMs; TIGR00231; small GTP; 1.
ZW Pfam; Pfam00071; GTP-binding; Prenylation; Lipoprotein.
FT NP_BIND 10 17 GTP (BY SIMILARITY).
FT NP_BIND 57 61 GTP (BY SIMILARITY).
FT NP_BIND 116 119 GTP (BY SIMILARITY).
FT DOMAIN 32 40 EFFECTOR REGION (BY SIMILARITY).
FT LIPID 185 185 FARNESYL (BY SIMILARITY).
SQ SEQUENCE 188 AA; 21452 MW; AAB6C198B259865 CR64;

Query Match: 95.7%; Score 67; GI: Length 188
Best local similarity: 92.1%; Field No. 00044;
Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SPEDXXXXXXXXXX 14
DB 171 SEDGXXXXXXXXXX 184

RESULT 4
PASK_CYPCA STANDARD; PRT; 188 AA.
AC Q9YH38; 2000 (rel. 39, Created:
DT 30-MAY-2000 (rel. 39, Last sequence update:
DT 16-OCT-2001 (rel. 40, Last annotation update:
DE Transforming protein p21 (K-Ras) (K1-Pas).
GN KRAS.
OS Cyprinus carpio (Common carp).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Cyprinus.
OX NCBI_TaxID-7962;
RN [1]
RP SEQUENCE FROM N.A.
RA Chang M S, Chang Y, Chang G D, Huang F H, Hwang H J,
PT "Molecular cloning and sequencing of two carp cDNAs encoding ras
PT related proteins."
PI submitted (Appended to the EMBL/GenBank/DBP databases)
TI FUNCTION: RAS (RAS) IS A GTP-BINDING PROTEIN THAT
CC ACTIVITY.
CC -- PRTYPE REGULATION: ALTERNATE BETWEEN AN INACTIVE FORM BOUND TO GDP
CC AND AN ACTIVE FORM BOUND TO GTP. ACTIVATED BY A KINASE
CC NUCLEOTIDE-EXCHANGE FACTOR (GEF) AND INACTIVATED BY A PHASE-
CC ACTIVATING PROTEIN (GAP).
CC -- SIMILARITY: BELONGS TO THE SMALL GTPASE SUPERFAMILY. RAS FAMILY.
CC
CC This SWISS-PROT entry is copyrighted. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation
CC the European Bioinformatics Institute. There are no restrictions on the
CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@sib-sib.ch).

DR EMBL; U53782; AAC05839.1; --
DR HSSP; P01112; IPLL.

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DR InterPro, IPR001077, GTPase Ras.
DR InterPro, IPR001260, Protein size.
DR InterPro, IPR001866, Ras transmem.
DR InterPro, IPR001245, Small_GTP.
DR Pfam, PF00071, Ras_1.
DR PRINTS, PR00449, RASTRANSFMNG.
DR SMART, SM00173, RAS, 1.
DR TIGRFAMs, TIGR00231, small GTP, 1.
KW PROTO-ONCOGENE, GTP-BINDING, GTP (BY SIMILARITY).
FT NP_BIND 16 17 GTP (BY SIMILARITY).
FT NP_BIND 57 61 GTP (BY SIMILARITY).
FT NP_BIND 116 119 GTP (BY SIMILARITY).
FT DOMAIN 32 40 EFFECTOR REGION (BY SIMILARITY).
FT LIPID 185 185 FARNESYL (BY SIMILARITY).
FT SEQUENCE 188 AA, 21454 MW, 255218DAP359650 CRC64.

Query Match 94.3%; Score 66; DB 1; Length 188;
Best Local Similarity 92.9%; Pred No. 0.061;
Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEQGKKKKKKSKTK 14
   |||
DB 171 SEQGKKKKKKSKTK 194
   |||

RESULT 5
RASK ORYLA
IT FACP CYTCA STANDARD, FFT, 189 AA
AC C42267,
DT 30 MAY-2000 (Rel. 39, Created)
DT 30 MAY-2000 (Rel. 39, Last sequence update)
DT 30 MAY-2000 (Rel. 39, Last sequence update)
CE Transformed from the FACP/Ras-1 cDNA by the
GN KRAC1.
OS Crinia latipes (Medaka fish) (Anura: Teleostei)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Clupeiformes; Teleostei; Euteleostei;
OC Acanthopterygii; Atherinomorpha; Atherinomorpha; Atherinomorpha;
OC Belontiiformes; Atherinomorpha; Atherinomorpha; Atherinomorpha;
OC Belontiiformes; Atherinomorpha; Atherinomorpha; Atherinomorpha;
CX RefSeq:AF030545.
RN [1]
SE SEQUENCE FROM N.A.
RP TISSUE=Liver;
SA Clepper, G.A., Van Beneden, S.J.,
RT Volting of rat liver cDNA sequences and a putative pseudogene
RL Submitted (Oct 1997) to the EMBL/GenBank/DDBJ databases
CC 1. FURTHER INFORMATION: RAS PROTEIN BIND 31/371 AND P00880 INTRINSIC GTPASE
CC ACTIVITY.
CC 2. ENZYME REGULATION: ALTERNATE BETWEEN AN INACTIVE FORM BIND TO GTP
CC AND AN ACTIVE FORM BIND TO GTP. ACTIVATED BY A GUANINE
CC NUCLEOTIDE EXCHANGE FACTOR (GEF) AND INACTIVATED BY A GTPASE-
CC ACTIVATING PROTEIN (GAP).
CC 3. SIMILARITY: BELONGS TO THE SMALL GTPASE SUPERFAMILY RAS FAMILY.
CC
CC THIS SWISS-PROT entry is identical to the one in the database.
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in the
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement. (See http://www.ebi.ac.uk/submit/submit.html
CC or send an email to license@ebi.ac.uk.)
CC
DR EMBL; AF030545; AAB86487.1; -.
DR RSR; F01117.f111.
DR InterPro, IPR001077, GTPase Ras.
DR InterPro, IPR001245, Small_GTP.
DR PRINTS, PR00449, RASTRANSFMNG.
DR SMART, SM00173, RAS, 1.
DR TIGRFAMs, TIGR00231, small GTP, 1.

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KW Farnesyl transferase, GTP-BINDING, Proto-oncogene, GTPase, Protein.
FT NP_BIND 16 17 GTP (BY SIMILARITY).
FT NP_BIND 57 61 GTP (BY SIMILARITY).
FT NP_BIND 116 119 GTP (BY SIMILARITY).
FT DOMAIN 32 40 EFFECTOR REGION (BY SIMILARITY).
FT LIPID 185 185 FARNESYL (BY SIMILARITY).
FT SEQUENCE 188 AA, 21450 MW, 2421871AA4722A0 CRC64.

Query Match 94.3%; Score 66; DB 1; Length 188;
Best Local Similarity 92.9%; Pred No. 0.061;
Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEQGKKKKKKSKTK 14
   |||
DB 171 SEQGKKKKKKSKTK 184
   |||

RESULT 6
RASK MOUSE
IT RASK MOUSE STANDARD; PRT; 188 AA.
AC P08643; P04200;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Transforming protein p21b (K-Ras 2b) (K-Ras) (p21b).
GN KRAS2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CX NCBI_TaxID=10090;
RN [1]
SE SEQUENCE FROM N.A.
RP GEORGE, D.L., SCOTT, A.F., TRUSKO, S.J., GLICK, B., FORD, E., DORNEY, D.C.;
RT "Structure and expression of amplified K-ras gene sequences in Y1
RT mouse adrenal tumor cells."
RT Science 225:1159-1162(1984).
RN [2]
SE SEQUENCE OF 1-37 FROM N.A.
RP MEDLINE:8306529; PubMed:17474163;
RA Guerrero I., Villasante A., Corces V., Pellicer A.;
RT "Activation of a K-ras oncogene by somatic mutation in mouse
RT lymphomas induced by gamma radiation."
RT Science 225:1159-1162(1984).
RN [3]
SE SEQUENCE OF 1-103 FROM N.A.
RP MEDLINE:9135529; PubMed:2547997;
RA George D.L., Scott A.F., Trusko S.J., Glick B., Franke U.;
RT "Amplified DNA in Y1 mouse adrenal tumor cells: isolation of cDNA
RT complementary to an amplified K-ras gene and localization of
RT coding and regulatory regions to mouse chromosome 6."
RT Nucleic Acids Res 12:3791-3794(1984).
RN [4]
RP REVIEW.
RP MEDLINE=87297453; PubMed=3304147;
RA Barltis W.
RT "Ras genes."
RP Annu Rev Biochem 56:799-827(1987).
CC 1. FUNCTION: RAS PROTEIN BIND GTP/GDP AND P00880 INTRINSIC GTPASE
CC ACTIVITY.
CC 2. ENZYME REGULATION: ALTERNATE BETWEEN AN INACTIVE FORM BIND TO GTP
CC AND AN ACTIVE FORM BIND TO GTP. ACTIVATED BY A GUANINE
CC NUCLEOTIDE EXCHANGE FACTOR (GEF) AND INACTIVATED BY A GTPASE-
CC ACTIVATING PROTEIN (GAP).
CC 3. ALTERNATIVE SPLICING: 2 ISOFORMS, A AND B, WHICH
CC DIFFER BY ALTERNATIVE SPLICING. THEY DIFFER IN THE C
CC TERMINAL REGION WITH IN ENDS BY TWO ALTERNATIVE EXONS (115 AND
CC 116).
CC 4. MAMMILIANS: THIS GENE IS AMPLIFIED IN THE MOUSE ADRENAL TUMOR
CC Y1 CELLS.
CC 5. MISCELLANEOUS: THE MAMMALIAN RAS GENE FAMILY CONSISTS OF THE
CC H-RAS, K-RAS, AND N-RAS. H-RAS, K-RAS, AND N-RAS ARE IN THE
CC PSEUDOGENE OF EACH (H-RAS, K-RAS, AND N-RAS) AND THE R-RAS GENE.

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gamma nucleotide-gated cation channel 1)
nated channel alpha subunit

data: Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Clariidae; Anis.

the EMBL/GenBank/DBJ databases

104499;
S. A. and G. M. A. (1999) Ray K.
r. cAMP-gated channel protein alpha-subunit:
n of the gene and characterization of the

1327
NACT TRANSDUCTION IS MEDIATED BY A G-PROTEIN
C-TERMINAL AS SECOND MESSANGERS. THE G-PROTEIN CAN
IC-TERMINAL WHICH LEADS TO A DEGRADATION OF THE CATION
CHANNEL A DEGRADATION OF THE CATION

OR HIGHER OLIGOMER.

in integral membrane protein
TO THE CYCLIC NUCLEOTIDE GATED CATION CHANNEL

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DR InterPro: IPR000504; RNA_rec_mot.
 DR InterPro: IPR000923; Znf_C2H2.
 DR InterPro: IPR001876; Znf_FanGDP.
 DR Pfam: PF00076; rrm; 2.
 DR Pfam: PF00096; zf_CCH2; 1.
 DR Pfam: PF00641; zf-RanBP; 1.
 DR Pfam: PF01585; G_patch; 1.
 DR SMART: SM00443; G_patch; 1.
 DR SMART: SM00360; RRM; 2.
 DR SMART: SM00355; Znf_C2H2; 1.
 DR SMART: SM00547; Znf_RRZ; 1.
 DR PROSITE: PS50174; G_PATCH; 1.
 DR PROSITE: PS50102; RRM; 2.
 DR PROSITE: PS00030; RRM_RNP1; 2.
 DR PROSITE: PS03358; ZF_RANBP2_1; 1.
 DR PROSITE: PS50199; ZF_RANBP2_2; 1.
 EF F0331E, F551157, ZNF_FINGER_C2H2; 1.
 KW Anti-origene; RNA-binding; Nucleic protein; Zinc finger; Repeat.
 FT DOMAIN aa 178
 FT ZN_FING 181 210 RANBP2 TYPE. RNA BINDING (PPM) 1.
 FT DOMAIN 231 315 RNA-BINDING (PPM) 2.
 FT ZN_FING 647 677 C2H2-TYPE (ATYPICAL).
 FT DOMAIN 743 789 G-PATCH.
 FT CONFLICT 53 54 DY -> GS (IN REF. 1).
 FT CONFLICT 354 354 G -> V (IN REF. 1).
 FT CONFLICT 455 455 MISSING (IN REF. 6).
 FT CONFLICT 788 788 G -> A (IN REF. 6).
 FT CONFLICT 812 812 T -> I (IN REF. 1).
 SQ SEQUENCE 815 AA, 92153 MW, AA799C2D13405479 QRC64;

Query Match 65.78; Score 46; DB 1; Length 815;
 Best Local Similarity 57.18; Pref No 15;
 Matches 8; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1 SXDGKYYKYYKSKY 14
 :|:|:|:|:|:|:
 DB 522 AVEGKREKREKPKSK 535

Search completed: March 3, 2003, 06:46:21
 Job time : 5.95122 secs


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UR InterPro: IFS005225; Small_GTP.
UP Pfam: PF00071; Ras; 1
UP PRINTS: P00040, PASTRP00000.
UP SMART: SM00173, PAS. 1.
UP TIGRfam: TIGR00231; Small_GTP; 1.
UP PROSITE: PS00004, PFT00010, TIGR00001.
UP PROSITE: PS00004, PFT00010, TIGR00001.
UP GTP-binding; Lipopeptide; Prenylation_1.
UW SEQUENCE 189 AA, 21443 MW, 64364.000, PIRAC CRC64;

Query Match 24/31 Score 667 DR 13; Length 189;
Best Local Similarity 20.93; E-Val. No. 0.016;
Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps
3

C7 1 STGTGYYVYVYVYV 14
   ||| ||| ||| |||
C8 1 STGTGYYVYVYVYV 184

RESULT 4
UPSS8
I2 QPSS8 PRELIMINARY; PPT: 188 AA.
AC QPSS8
DT 01-MAY-2000 (TRENRE1.13, Created)
DT 01-MAY-2000 (TRENRE1.13, Last sequence update)
DI 01-MAY-2000 (TRENRE1.13, Last annotation update)
DE Pol-ras protein.
GN
KI PAS.
OS Placithrus flossus (European flounder).
OC Eukaryota; Metazoa; Chordata; Teleostei; Perciformes;
OC Actinopterygii; Acipenseriformes; Teleostei; Perciformes;
OC Acanthopterygii; Acanthopterygii; Perciformes; Perciformes;
OC Placithridae; Placithridae; Placithridae; Placithridae;
OC NCBI TAXID=9250;

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RI      Cyt B1-1c 897871 P. R1-seq. M1 Plac 12617127-200000
CC -1- SIMILARITY: REFINGS TO THE SMALL GTPASE SUPERFAMILY PAS FAMILY.
DR EMBL: V17187; CAA766678.1; ..
DR HSSP: P01312; 1PLL.
DR InterPro: IPR003577; GTPase_Pas.
DR InterPro: IPR001230; Proxyl_site.
CC Interflic: IPR003606; Bas_tig_singlmg.
DR InterPro: IPR003225; Small_GTP.
DR Pfam: PF00071; ras; 1.
DR PRINTS: PF00449; FASTIPRHRMG.
DR SMART: SM00173; PAS; 1.
CC TIGRfam: TIGR00222; SmallGTP; 1.
DR EPRINT: F00294; FERMATIN; UNKNOWN 1.
FW GTP-binding; EF00256; ProteinAtlas.
CC SEQUENCE 188 AA, 1140 MW, 18166 Da, pI 5.64;

      Query Match          100%   Score 26.00  E-13.0  100% 100%
      Positional similarity: 100%, Posit Neg Ratio: 0.000000
      Matches: 15, Identicalities: 15, Mismatches: 0, Indels: 0, Gaps: 0

QY       1 SKDGKFKKKFKSKTY 14
ID       171 SKDGKFKKKFKSKTK 184
        |||:|||||
        |||:|||||

RESULT 5
C82954
AC C82954;
DT 01-NOV-1995 (TrEMBLrel_01, Created)
DT 01-NOV-1995 (TrEMBLrel_01, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel_01, Last annotation update)
DE Proto-oncogene protein.
DS Kirsten murine sarcoma virus.
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Query Match 75-78, 55-59, pp 11, length 930;

Tab time : 33.3932 secs

EA Glick A., Egan P., Gurell J. H., Gu J., Guo F., Harris M.,
 RA Harris N.L., Harvey D., Heiman T. J., Hernandez J. P., Houck J.,
 RA Hostin D., Houston K. A., Howland T. J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Keanison A., Kerchum K.A.,
 RA Kimmel B.E., Kodira C. D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Laske P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M. P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson C.E., Nelson K.A., Nixon K., Nusskern D. P., Pacleb J. M.,
 EA Palacelis M., Pittman G.S., Pan S., Peillard J., Puri V., Reese M. G.,
 RA Reinert K., Remington K., Sanders P.D.C., Scheeler P., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A. C., Stapleton M., Strong R., Sun F.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissenbach J.,
 RA Williams S.M., Woodage T., Worley K. C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yen R. F., Zaveri J.S., Zhang X., Zhang G., Zhao C., Zheng L.,
 RA Zhou X.H., Zhou F. H., Zhou W., Zhou X., Zhu S., Zhu X., Smith H. O.,
 RA Gibbs P.A., Myers E.W., Rubin G. M., Venter J.C.,
 RT "The genome sequence of Drosophila melanogaster."
 E1 C010558 287 2185 C105 (2000).
 DP EMBL: AE003493; AAF49307 1;
 DR FlyBase: FBgn0001087; g.
 DR InterPro: IPR002553; Adaptin_N.
 DR Pfam: PF01602; Adaptin_N; 1.
 SQ SEQUENCE 568 AA; 63011 MW; C4F1507AAAR07AA CRC64;

Query Match 71.4%; Score 50; DB 5; Length 568;
 Best Local Similarity 83.3%; Pred. No. 9 9;
 Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 SKDCKKPKKPK 12
 |||||
 DE 493 SKDCKKPKKPK 504

RESULT 15
 045031
 ID 045031 PRELIMINARY; PRT: 810 AA.
 AC 045031;
 DT 01-JUN-1998 (TrEMBLrel 06, Created)
 DI 01-JUN-1998 (TrEMBLrel 06, Last sequence update)
 DT 01-JUN-2001 (TrEMBLrel 17, Last annotation update)
 DE Delta adaptin subunit of AP-3.
 OS G OR GARNER OR CG10956 OE CG11197.
 OS Drosophila melanogaster (fruit fly).
 CC Eukaryota; Metazoa; Arthropoda; Insecta;
 CC Euryptera; Neptera; Euryptera; Diptera; Prichytera; Muscomorpha;
 CC Ephyra; Ephyra; Ephyra; Ephyra; Ephyra; Ephyra;
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N A
 RC STRAIN=OREGON;
 RA Lloyd V.K., Sinclair D.A., Weinberg P., Warner T.S., Honda R.M.,
 RA Grigliatti T.A.; (seq) to the EMBL/GenBank/DBPI databases
 RL Submitted (JAN 1998) to the EMBL/GenBank/DBPI databases
 DE EMBL: AF044287; AAC01743.1;
 DE FlyBase: FBgn0001087; g.
 DE InterPro: IPR002553; Adaptin_N
 DE Pfam: PF01602; Adaptin_N; 1;
 SQ SEQUENCE 410 AA; 40666 MW; E3010657R98R064R CRC64;

Query Match 71.4%; Score 50; DB 5; Length 810;
 Best Local Similarity 83.3%; Pred. No. 14;
 Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 SKDCKKPKKPK 12
 |||||
 DE 493 SKDCKKPKKPK 733

XX PS Claim 11; Page 70; 75pp; English.

XX CC The present peptide sequence represents a specifically claimed membrane

XX CC binding element. The invention relates to a soluble derivative (A) of a

XX CC soluble polypeptide (I), which comprises at least 2 heterologous

XX CC membrane-binding elements (MKE) of low membrane affinity covalently

XX CC associated with (i) MRE interact, independently and with thermodynamic

XX CC affinity, with components of cellular or artificial membranes exposed

XX CC to vitellin; (ii) (A) are used to treat disorders treatable with

XX CC (i) itself, specifically inflammation or any other complement-related

XX CC disorder (e.g. connective tissue, great vessel, or arterial

XX CC infarction, sepsis, thrombotic arthritis and many others, including

XX CC application to swelling liver and antithrombotic disorders, but also

XX CC treatment to induce weight loss, to treat ischaemia or asthma and as

XX CC immune modulators for treating multiple sclerosis (A) are administered

XX CC orally, topically, by injection or inhalation at 0.1 to preferably

XX CC 0.1-10) mg/kg/day.

XX CC Sequence 14 AA,

XX CC Query Match 100.0%; Score 70; DP 19; Length 14;

XX CC Best Local Similarity 100.0%; Pred. No. 0.00042;

XX CC Matches 14; Conservation 0; Mismatches 0; Indels 0; Gaps 0;

XX CC 1 CFFGKPPPPKPPK 14

XX CC 1 CFFGKPPPPKPPK 14

XX CC RESULT 2

XX CC ID ABB91241 standard; peptide; 14 AA.

XX CC AC ABB91241;

XX CC DT 20 AUG 2002 (first entry)

XX CC DE Antibacterial membrane binding peptide SEQ ID NO 9

XX CC KW Antibacterial, glycopeptide, peptide membrane associated element,

XX CC KW bacterial infection; vancomycin; peptidoglycan biosynthesis inhibition,

XX CC KW antibiotic.

XX CC OS Synthetic.

XX CC PN WC00236612 A1.

XX CC PD 10 MAY 2002.

XX CC PF 02 NOV 2001; 2601W5 GP0467

XX CC PR 03 NOV 2000; 2000RP 002624.

XX CC PA (UYCA-) UNIV CAMBRIDGE TECH SERVICES LTD.

XX CC PA (ADPR-) ADPRUTECH LTD.

XX CC PI Couplé X5, Beller CE,

XX CC DP WPI; 2002 471499/50.

XX CC PT Antibacterial compound, useful for the treatment of a bacterial

XX CC PT infection by sub-gram positive or negative bacteria, peptides 9

XX CC PT conjugate of gly-peptide and peptide membrane associating element

XX CC PS Claim 7; Page 57; 64pp; English.

XX CC The present invention describes an antibacterial compound (I), comprising

XX CC a conjugate of glycopeptide and peptide membrane associating element

XX CC (I) comprises the formula V, X, where V is a glycopeptide moiety that

XX CC inhibits peptidoglycan biosynthesis in bacteria, X is a linking group,

XX CC W is a peptide membrane associating element, and X = H or a membrane

XX CC insertive element. Also described is (i) a method of treating or preventing

XX CC a bacterial infection, comprising the administration of (I) and (ii) use

XX CC of (I) in the manufacture of a medicament for the treatment or prevention

XX CC of a bacterial infection. (I) are used in the manufacture of a medicament

XX CC for the treatment or prophylaxis of a bacterial infection in a human or

XX CC animal body, including both the upper digestive and gram negative bacteria

XX CC including *Mycobacterium* sp., *Enterococcus* sp., *Escherichia* sp.,

XX CC *Staphylococcus* sp., *Vibrio* sp., *Helicobacter* sp., *Parvella* sp., *Klebsiella*

XX CC sp., *Hemophilus* sp., *Clostridium* sp., *Pseudomonas* sp., *Actinomyces* sp.,

XX CC *Proteus* sp. or *Salmonella* sp. particularly antibiotic resistant

XX CC bacterial strains. (I) are also useful as wound treatment agents to

XX CC prevent bleeding of bacteria in medical devices, especially for teeth,

XX CC exposed in wound tissues, and for prophylactic use in dental treatment as

XX CC an alternative to oral or subcutaneous treatment with antibiotic prophylaxis.

XX CC has stronger binding to bacterial membrane which have a higher

XX CC content of acidic phospholipids than the eukaryotic membrane, also

XX CC having a higher proportion of membrane associated fluorescent proteins.

XX CC Various in vivo experiments and in vitro activity have demonstrated

XX CC with (I) and is effective to treat the antibiotic resistant bacterial

XX CC strains. ABB91234 to ABB91242 represent peptides given in the

XX CC exemplification of the present invention.

XX CC Sequence 14 AA,

XX CC Query Match 100.0%; Score 60; DP 23; Length 14;

XX CC Best Local Similarity 100.0%; Pred. No. 0.00042;

XX CC Matches 14; Conservation 0; Mismatches 0; Indels 0; Gaps 0;

XX CC 1 CFFGKPPPPKPPK 14

XX CC 1 CFFGKPPPPKPPK 14

XX CC RESULT 3

XX CC ID AAW45893 standard; peptide; 15 AA.

XX CC AC AAW45893;

XX CC DT 30 JUN 1999 (first entry)

XX CC DE Peptide membrane binding element.

XX CC KW Membrane binding element, thrombotic disease, soluble protein;

XX CC KW complement-related disease; integral membrane protein; inflammation.

XX CC OS Synthetic.

XX CC PN WO9802454-A2.

XX CC PD 22 JAN 1998.

XX CC PF 08 JUL 1997; 97WO-EP03715.

XX CC PP 15 JUL 1996; 96GR-0014871.

XX CC PA (ADPR-) ADPRUTECH PLC.

XX CC PI Couplé X5, Beller CE, Smith RAG;

XX CC DP WPI; 1998 110524/10.

XX CC PT Derivatives of soluble polypeptide(s) bonded to low affinity

XX CC membrane binding group, useful for treating complement related and

XX CC thrombotic diseases, providing improved localization at cellular

XX CC membranes

XX CC PS Claim 21; Page 71; 75pp; English.

XX CC The present peptide sequence represents a specifically claimed membrane

XX CC binding element. The invention relates to a soluble derivative (A) of a

XX CC soluble polypeptide (I), which comprises at least 2 heterologous

XX CC membrane-binding elements (MKE) of low membrane affinity covalently

XX CC associated with (i) MRE interact, independently and with thermodynamic

... of collagen ... membranes exposed ...
... are used to treat disorders treatable with ...
... inflammation of any other complement related ...
... disease, graft rejection, myocardial ...
... and arthritis and many others; including ...
... (devices) and thereby to disease, but also to ...
... with loss, to treat ischemia or asthma and as ...
... treating multiple sclerosis. AA are administered ...
... by injection or inhalation at 0.01-10 (preferably ...

Query Match 100.0%; Score 70; DB 1; Length 15;
Best Local Similarity 100.0%; Pred No 0.0044;
Matches 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SKDGGKYYKSKTK 14
DB 1 SKDGGKYYKSKTK 14

RESULT 5
AAP60118
ID AAP60118 standard; protein: 16 AA.
XX
AC AAP60118;
DT 01-JAN-1980 (first entry)
XX
DE K4B-ras p21 oncogene protein (170-185).
XX
KW Ras oncogene; monoclonal antibody; polyclonal anti-p21; Ras has
XX p21 ras oncogene, immunometric assay; tumor; cancer; etc.
XX
OS Synthetic.
XX
XX EP203587-A.
XX
PD 03-DEC-1986.
XX
RF 26-MAY-1986; 86EP-0107244.
XX
FR 30-MAY-1986; 86US-0739416.
XX
PA (HOFF) HOFFMANN-LA ROCHE AG.
XX
PI Chizzonite RA, Felix AM, Furth ME;
XX
DR WPI; 1986-320542/49.
XX
XX
PT New ras oncogene poly peptide(s) - used for protein antibodies
PT for immunometric assays for presence of p21 ras oncogene family
XX
XX
PS Claim 1; page 22; 28pp; English.
XX
XX

This sequence represents the H-ras p21 protein (170-185). It may be
covalently linked to an immunogenic carrier to produce antibodies
which are specific to the ras oncogene from which the polypeptide is
derived. The antibodies may be used in immunoassays to determine
the presence of each individual p21 ras oncogene family member. The
proteins are preferably produced by solid-phase synthesis. See also
AAP60114-17.

Query Match 100.0%; Score 70; DB 1; Length 16;
Best Local Similarity 100.0%; Pred No 0.0047;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SKDGGKYYKSKTK 14
DB 2 SKDGGKYYKSKTK 15

RESULT 6
AAP60118
ID AAP60118 standard; protein: 16 AA.
XX
AC AAP60118;
DT 01-JAN-1980 (first entry)
XX
DE K4B-ras p21 oncogene protein (170-185).
XX
KW Ras oncogene; monoclonal antibody; polyclonal anti-p21; Ras has
XX p21 ras oncogene, immunometric assay; tumor; cancer; etc.
XX
OS Synthetic.
XX
XX EP203587-A.
XX
PD 03-DEC-1986.
XX
RF 26-MAY-1986; 86EP-0107244.
XX
FR 30-MAY-1986; 86US-0739416.
XX
PA (HOFF) HOFFMANN-LA ROCHE AG.
XX
PI Chizzonite RA, Felix AM, Furth ME;
XX
DR WPI; 1986-320542/49.
XX
XX
PT New ras oncogene poly peptide(s) - used for protein antibodies
PT for immunometric assays for presence of p21 ras oncogene family
XX
XX
PS Claim 1; page 22; 28pp; English.
XX
XX

This sequence represents the H-ras p21 protein (170-185). It may be
covalently linked to an immunogenic carrier to produce antibodies
which are specific to the ras oncogene from which the polypeptide is
derived. The antibodies may be used in immunoassays to determine
the presence of each individual p21 ras oncogene family member. The
proteins are preferably produced by solid-phase synthesis. See also
AAP60114-17.

Query Match 100.0%; Score 70; DB 1; Length 16;
Best Local Similarity 100.0%; Pred No 0.0047;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;


```

1 CURRENT FILING DATE: 2001-03-26
2 PRIOR APPLICATION NUMBER: 60/181,496
3 PRIOR FILING DATE: 2001-04-04
4 PRIOR APPLICATION NUMBER: 60/178,761
5 PRIOR FILING DATE: 2001-03-27
6 PRIOR APPLICATION NUMBER: 60/146,755
7 PRIOR FILING DATE: 1998-08-04
8 PRIOR APPLICATION NUMBER: 69/817,144
9 PRIOR FILING DATE: 2001-03-27
10 PRIOR APPLICATION NUMBER: 69/196,139
11 PRIOR FILING DATE: 1994-02-17
12 NUMBER OF SEQ ID NOS: 193
13 SOFTWARE: PatentIn 2.1
14 SEQ ID NO: 89
15 LENGTH: 18
16 TYPE: PRT
17 ORGANISM: Homo sapiens
18 US-09-984-056-89

```

```

Query Match 85.7%; Score 60; DB 10; Length 18;
Best Local Similarity 100.0%; Pred No. 0.049;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QV 1 SKDQKFFKSK 12
   |||||
Db 7 SKDQKFFKSK 18

```

```

RESULT 3
US-09-984-057-89
1 Sequence 89, Application US/09984057
2 Patent No. US6360315/79A
3 GENERAL INFORMATION:
4 APPLICANT: BOGUCH, SAMUEL
5 TITLE OF INVENTION: RELAXINS AND METHODS OF IDENTIFYING
6 FILE REFERENCE: 6945-249-84
7 CURRENT APPLICATION NUMBER: 68/004944,057
8 CURRENT FILING DATE: 2001-10-26
9 PRIOR APPLICATION NUMBER: 60/163,390
10 PRIOR FILING DATE: 2001-07-09
11 PRIOR APPLICATION NUMBER: 69/196,139
12 PRIOR FILING DATE: 2001-03-27
13 PRIOR APPLICATION NUMBER: 69/146,755
14 PRIOR FILING DATE: 1998-08-04
15 PRIOR APPLICATION NUMBER: 69/817,144
16 PRIOR FILING DATE: 2001-03-27
17 PRIOR APPLICATION NUMBER: 69/196,139
18 NUMBER OF SEQ ID NOS: 90
19 SOFTWARE: PatentIn 2.1
20 SEQ ID NO: 89
21 LENGTH: 18
22 TYPE: PRT
23 ORGANISM: Homo sapiens
24 US-09-984-057-89

```

```

Query Match 85.7%; Score 60; DB 10; Length 18;
Best Local Similarity 100.0%; Pred No. 0.049;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QV 1 SKDQKFFKSK 12
   |||||
Db 7 SKDQKFFKSK 18

```

```

RESULT 4
US-09-945-249-84
1 Sequence 84, Application US/09045249
2 Patent No. US6200101/84A1
3 GENERAL INFORMATION:
4 APPLICANT: BERLIN, VIVIAN

```

```

1 APPLICANT: DANARNEZ, VERONIQUE
2 APPLICANT: SMITH, SIOBHAN E
3 TITLE OF INVENTION: ASSAYS AND REAGENTS FOR IDENTIFYING ANTI-FETAL ANTIBODIES,
4 TITLE OF INVENTION: ASSAYS AND REAGENTS FOR IDENTIFYING ANTI-FETAL ANTIBODIES,
5 FILE REFERENCE: MIV-074-06
6 CURRENT APPLICATION NUMBER: US/09/045,249
7 CURRENT FILING DATE: 2001-08-31
8 PRIOR APPLICATION NUMBER: 60/041,950
9 PRIOR FILING DATE: 2001-01-13
10 PRIOR APPLICATION NUMBER: 08/771,212
11 PRIOR FILING DATE: 1996-12-20
12 PRIOR APPLICATION NUMBER: 08/631,419
13 PRIOR FILING DATE: 1996-04-11
14 NUMBER OF SEQ ID NOS: 89
15 SOFTWARE: PatentIn Ver. 2.1
16 SEQ ID NO: 84
17 LENGTH: 15
18 TYPE: PRT
19 ORGANISM: Artificial Sequence
20 FEATURE:
21 OTHER INFORMATION: Description of Artificial Sequence: Reptide that
22 OTHER INFORMATION: corresponds to the C-terminal of protein of interest
23 OTHER INFORMATION: substrates
24 US-09-945-249-84

```

```

Query Match 78.6%; Score 55; DB 9; Length 15;
Best Local Similarity 100.0%; Pred No. 0.049;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QV 4 GPKKFKFKFK 14
   |||||
Db 1 GPKKFKFKFK 11

```

```

RESULT 5
US-09-784-819-2
1 Sequence 2, Application US/090784818
2 Publication No. US6000102/93A1
3 GENERAL INFORMATION:
4 APPLICANT: Merck & Co., Inc.
5 APPLICANT: Eisenberg, Christopher J.
6 APPLICANT: Bergman, Jeffrey M.
7 TITLE OF INVENTION: PEPTIDE PROTEIN TRANSFERASE INHIBITORS
8 FILE REFERENCE: 20496
9 CURRENT APPLICATION NUMBER: 09/0784,818
10 CURRENT FILING DATE: 2001-02-16
11 PRIOR APPLICATION NUMBER: 60/181,451
12 PRIOR FILING DATE: 2000-02-19
13 NUMBER OF SEQ ID NOS: 21
14 SOFTWARE: FastSeq for Windows Version 4.0
15 SEQ ID NO: 2
16 LENGTH: 15
17 TYPE: PRT
18 ORGANISM: Artificial Sequence
19 FEATURE:
20 OTHER INFORMATION: completely synthesized sequence
21 US-09-784-819-2

```

```

Query Match 78.6%; Score 55; DB 9; Length 15;
Best Local Similarity 100.0%; Pred No. 0.049;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QV 4 GPKKFKFKFK 14
   |||||
Db 1 GPKKFKFKFK 11

```

```

RESULT 6
US-09-770-967-2
1 Sequence 2, Application US/090770967
2 Patent No. US6200101/84A1
3 GENERAL INFORMATION:
4 APPLICANT: Merck & Co., Inc.

```

us-09-214-913-41.rapb

3 2003

Mar 3

; PRIOR APPLICATION NUMBER: US 60/111,416
 ; PRIOR FILING DATE: 1998-12-08
 ; PRIOR APPLICATION NUMBER: US 60/129,282
 ; PRIOR FILING DATE: 1999-04-14
 ; NUMBER OF SEQ ID NOS: 21
 ; SOFTWARE: FASTSEQ for Windows Version 3.0
 ; SEQ ID NO 2
 ; LENGTH: 15
 ; TYPE: PRT
 ; ORGANISM: Homosapien
 ; US 09-214-913-41-2
 Query Match 78.6%; Score 55; DB 10; Length 15
 Best Local Similarity 100.0%; Pred. No. 0.049;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0
 QY 4 GPPYYVYSYTK 14
 LB 1 GPPYYVYSYTK 11
 RESULT 9
 US-09-757-251-3
 ; Sequence 3, Application US/09757251
 ; Patent No. US666049217A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Merck & Co., Inc.
 ; APPLICANT: S. Jane desOlas
 ; APPLICANT: Suzanne C MacTough
 ; APPLICANT: Anthony W. Shaw
 ; TITLE OF INVENTION: INHIBITORS OF PRENYL-PROTEIN TRANSFERASE
 ; FILE REFERENCE: 20604Y
 ; CURRENT APPLICATION NUMBER: US/09/757,251
 ; CURRENT FILING DATE: 2001-01-09
 ; PRIOR APPLICATION NUMBER: 60/175,784
 ; PRIOR FILING DATE: 2000-01-12
 ; NUMBER OF SEQ ID NOS: 25
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 3
 ; LENGTH: 15
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Completely Synthetic Amino Acid
 ; US-09-757-251-3
 Query Match 78.6%; Score 55; DB 10; Length 15
 Best Local Similarity 100.0%; Pred. No. 0.049;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0
 QY 4 GPPYYVYSYTK 14
 LB 1 GPPYYVYSYTK 11
 RESULT 10
 US-09-784-897A-2
 ; Sequence 2, Application US/09784897A
 ; Patent No. US666053343A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Merck & Co., Inc.
 ; APPLICANT: Binsmore, Christopher J.
 ; APPLICANT: Bergman, Jeffrey M.
 ; TITLE OF INVENTION: PRENYL-PROTEIN TRANSFERASE INHIBITORS
 ; FILE REFERENCE: 20497
 ; CURRENT APPLICATION NUMBER: US/09/784,897A
 ; CURRENT FILING DATE: 2001-06-20
 ; PRIOR APPLICATION NUMBER: 60/183,449
 ; PRIOR FILING DATE: 2000-02-18
 ; NUMBER OF SEQ ID NOS: 21
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 2
 ; LENGTH: 15

; PRIOR APPLICATION NUMBER: US 60/111,416
 ; PRIOR FILING DATE: 1998-12-08
 ; PRIOR APPLICATION NUMBER: US 60/129,282
 ; PRIOR FILING DATE: 1999-04-14
 ; NUMBER OF SEQ ID NOS: 21
 ; SOFTWARE: FASTSEQ for Windows Version 3.0
 ; SEQ ID NO 2
 ; LENGTH: 15
 ; TYPE: PRT
 ; ORGANISM: Homosapien
 ; US 09-214-913-41-2
 Query Match 78.6%; Score 55; DB 10; Length 15
 Best Local Similarity 100.0%; Pred. No. 0.049;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0
 QY 4 GPPYYVYSYTK 14
 LB 1 GPPYYVYSYTK 11
 RESULT 9
 US-09-757-251-3
 ; Sequence 3, Application US/09757251
 ; Patent No. US666049217A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Merck & Co., Inc.
 ; APPLICANT: S. Jane desOlas
 ; APPLICANT: Suzanne C MacTough
 ; APPLICANT: Anthony W. Shaw
 ; TITLE OF INVENTION: INHIBITORS OF PRENYL-PROTEIN TRANSFERASE
 ; FILE REFERENCE: 20604Y
 ; CURRENT APPLICATION NUMBER: US/09/757,251
 ; CURRENT FILING DATE: 2001-01-09
 ; PRIOR APPLICATION NUMBER: 60/175,784
 ; PRIOR FILING DATE: 2000-01-12
 ; NUMBER OF SEQ ID NOS: 25
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 3
 ; LENGTH: 15
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Completely Synthetic Amino Acid
 ; US-09-757-251-3
 Query Match 78.6%; Score 55; DB 10; Length 15
 Best Local Similarity 100.0%; Pred. No. 0.049;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0
 QY 4 GPPYYVYSYTK 14
 LB 1 GPPYYVYSYTK 11
 RESULT 10
 US-09-784-897A-2
 ; Sequence 2, Application US/09784897A
 ; Patent No. US666053343A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Merck & Co., Inc.
 ; APPLICANT: Binsmore, Christopher J.
 ; APPLICANT: Bergman, Jeffrey M.
 ; TITLE OF INVENTION: PRENYL-PROTEIN TRANSFERASE INHIBITORS
 ; FILE REFERENCE: 20497
 ; CURRENT APPLICATION NUMBER: US/09/784,897A
 ; CURRENT FILING DATE: 2001-06-20
 ; PRIOR APPLICATION NUMBER: 60/183,449
 ; PRIOR FILING DATE: 2000-02-18
 ; NUMBER OF SEQ ID NOS: 21
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 2
 ; LENGTH: 15

```
? TYPE: PRT
? ORGANISM: Artificial Sequence
? FEATURE:
? OTHER INFORMATION: Completely Synthetic Sequence
US-09-784-897A-2

Query Match          78.6%; Score 55; DB 10; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.049;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GYFFVYYSKTK 14
DB 1 GYFFVYYSKTK 11

RESULT 11
US-09-770-983-2
? Sequence 3, Application US/09770983
? Patent No. US6000005A1
? GENERAL INFORMATION:
? APPLICANT: Merck & Co., Inc.
? APPLICANT: Bergman, Christopher G.
? APPLICANT: Bergman, Jeffrey M.
? TITLE OF INVENTION: INHIBITORS OF PROTEIN PROTEIN TRANSFERASE
? FILE REFERENCE: 206367
? CURRENT APPLICATION NUMBER US/09/770,983
? PRIOR FILING DATE: 2001-04-17
? PRIOR APPLICATION NUMBER: 60/183,650
? PRIOR FILING DATE: 2000-02-18
? NUMBER OF SEQ ID NOS: 1
? SOFTWARE: FastSeq for Windows Version 4.0
? SEQ ID NO: 3
? LENGTH: 15
? TYPE: PRT
? ORGANISM: Homosapien
US-09-770-983-2

Query Match          78.6%; Score 55; DB 10; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.049;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GYFFVYYSKTK 14
DB 1 GYFFVYYSKTK 11

RESULT 12
US-09-828-325A-3
? Sequence 3, Application US/09828325A
? Patent No. US6000005A1
? GENERAL INFORMATION:
? APPLICANT: Merck & Co., Inc.
? APPLICANT: Craig A. Stump
? APPLICANT: Theresa M. Williams
? TITLE OF INVENTION: INHIBITORS OF PROTEIN-PROTEIN TRANSFERASE
? FILE REFERENCE: 206367
? CURRENT APPLICATION NUMBER US/09/828,325A
? CURRENT FILING DATE: 2001-08-17
? PRIOR FILING DATE: 2000-04-10
? PRIOR APPLICATION NUMBER: 60/196,044
? NUMBER OF SEQ ID NOS: 25
? SOFTWARE: FastSeq for Windows Version 4.0
? SEQ ID NO: 3
? LENGTH: 15
? TYPE: PRT
? ORGANISM: Artificial Sequence
? FEATURE:
? OTHER INFORMATION: Completely Synthetic Amino Acid
US-09-828-325A-3

Query Match          78.6%; Score 55; DB 10; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.049;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
? TYPE: PRT
? ORGANISM: Artificial Sequence
? FEATURE:
? OTHER INFORMATION: Completely Synthetic Sequence
US-09-757-217A-3

Query Match          79.4%; Score 55; DB 10; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.049;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GYFFVYYSKTK 14
DB 1 GYFFVYYSKTK 11

RESULT 13
US-09-757-217A-3
? Sequence 3, Application US/09757217A
? Patent No. US6000005A1
? GENERAL INFORMATION:
? APPLICANT: Merck & Co., Inc.
? APPLICANT: S. Jane deSolms
? APPLICANT: Gerald E. Stokker
? APPLICANT: Anthony W. Shaw
? TITLE OF INVENTION: INHIBITORS OF PROTEIN-PROTEIN TRANSFERASE
? FILE REFERENCE: 206371
? CURRENT APPLICATION NUMBER US/09/757,217A
? CURRENT FILING DATE: 2001-06-25
? PRIOR APPLICATION NUMBER: 60/176,801
? PRIOR FILING DATE: 2000-01-12
? NUMBER OF SEQ ID NOS: 25
? SOFTWARE: FastSeq for Windows Version 4.0
? SEQ ID NO: 3
? LENGTH: 15
? TYPE: PRT
? ORGANISM: Artificial Sequence
? FEATURE:
? OTHER INFORMATION: Completely Synthetic Amino Acid
US-09-757-217A-3

Query Match          79.4%; Score 55; DB 10; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.049;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GYFFVYYSKTK 14
DB 1 GYFFVYYSKTK 11

RESULT 14
US-09-828-259A-3
? Sequence 3, Application US/09828259A
? Patent No. US6000005A1
? GENERAL INFORMATION:
? APPLICANT: Merck & Co., Inc.
? APPLICANT: Diem N. Nguyen
? APPLICANT: Craig A. Stump
? APPLICANT: Theresa M. Williams
? TITLE OF INVENTION: INHIBITORS OF PROTEIN-PROTEIN TRANSFERASE
? FILE REFERENCE: 206371
? CURRENT APPLICATION NUMBER US/09/828,259A
? CURRENT FILING DATE: 2001-04-09
? PRIOR APPLICATION NUMBER: 60/196,044
? PRIOR FILING DATE: 2000-04-10
? NUMBER OF SEQ ID NOS: 25
? SOFTWARE: FastSeq for Windows Version 4.0
? SEQ ID NO: 3
? LENGTH: 15
? TYPE: PRT
? ORGANISM: Artificial Sequence
? FEATURE:
? OTHER INFORMATION: Completely Synthetic Amino Acid
US-09-828-259A-3

Query Match          79.4%; Score 55; DB 10; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.049;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GYFFVYYSKTK 14
DB 1 GYFFVYYSKTK 11
```





```
RESULT 2
US 08 564 164A 9
Sequence 9, Application US/08464164A
Patent No. 6109042
GENERAL INFORMATION:
APPLICANT: Schwabigheffer, Fabien
APPLICANT: Toque, Bruno
TITLE OF INVENTION: Intracellular Binding Proteins and Use
TITLE OF INVENTION: Title of
NUMBER OF SEQUENCES: 17
CURRENT INVENTION ADDRESS:
ADDRESS: 500 Arcadia Road, 3043
CITY: Collegeville
STATE: PA
COUNTRY: USA
ZIP: 19426 0107
COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
GENERATING SYSTEM: PC DOS/MS DOS
SOFTWARE: Patent Release #100, Version #1 30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08464164A
FILING DATE: 28-DEC-1995
CLASSIFICATION: 424
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: WO PCT/FR94/00714
FILING DATE: 19-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 94 3141
FILING DATE: 16-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Cavitzky, Martin F.
REGISTRATION NUMBER: 33,609
REFERENCE/DOCKET NUMBER: ST02030 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (610)454-3816
TELEFAX: (610)454 3808
INFORMATION FOR SEQ ID NO. 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-564-164A-9

Query Match
Best Local Similarity 100.0%, Prod No. 0.00000,
Matches 14, Conservative 0, Mismatches 0, Indels 0, Gaps 0

7 7 SEQID=FFFFFSTK 14
| | | | | | | | | |
DB 7 SEQID=FFFFFSTK 14

RESULT 3
US 08 564 164A 9
Sequence 6, Application US/08464164A
Patent No. 6109042
GENERAL INFORMATION:
APPLICANT: Schwabigheffer, Fabien
APPLICANT: Toque, Bruno
TITLE OF INVENTION: Intracellular Binding Proteins and Use
TITLE OF INVENTION: Title of
NUMBER OF SEQUENCES: 16
COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
GENERATING SYSTEM: PC DOS/MS DOS
SOFTWARE: Patent Release #100, Version #1 30 (EP)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08464164A
FILING DATE: 28-DEC-1995
CLASSIFICATION: 424
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: WO PCT/FR94/00714
FILING DATE: 19-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 94 3141
FILING DATE: 16-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Cavitzky, Martin F.
REGISTRATION NUMBER: 33,609
REFERENCE/DOCKET NUMBER: ST02030 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (610)454-3816
TELEFAX: (610)454 3808
INFORMATION FOR SEQ ID NO. 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-564-164A-9

Query Match
Best Local Similarity 100.0%, Prod No. 0.00000,
Matches 14, Conservative 0, Mismatches 0, Indels 0, Gaps 0

7 7 SEQID=FFFFFSTK 14
| | | | | | | | | |
DB 7 SEQID=FFFFFSTK 14

RESULT 4
US 08 439 964-34
Sequence 94, Application US/08439964
Patent No. 5302243
GENERAL INFORMATION:
APPLICANT: BROWN, MICHAEL S.
APPLICANT: GOLDSTEIN, JOSEPH L.
APPLICANT: BEISS, YUVAL
APPLICANT: JAMES, GUY L.
TITLE OF INVENTION: METHODS FOR THE IDENTIFICATION OF PARNESYL
NUMBER OF SEQUENCES: 95
CORRESPONDENCE ADDRESS:
ADDRESS: 10000, WHITE & DRYER
STREET: P O BOX 4433
CITY: HOUSTON
STATE: TEXAS
COUNTRY: UNITED STATES OF AMERICA
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC DOS/MS DOS/ASCII
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08439964
FILING DATE: 27-APR-1995
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US/08439964
FILING DATE: 16-FEB-1993
CLASSIFICATION: 435
APPLICATION NUMBER: US/07922,611
FILING DATE: APPOINTED
CLASSIFICATION: 435
APPLICATION NUMBER: US/07922,611
FILING DATE: 20-NOV-1990
CLASSIFICATION: 435
APPLICATION NUMBER: US/07922,611
FILING DATE: 19-APR-1990 (APPOINTED)
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: PARKER, DAVID L.
REGISTRATION NUMBER: 32,165
REFERENCE/DOCKET NUMBER: US/07922,611/PAR
TELECOMMUNICATION INFORMATION:
TELEPHONE: (610) 418-3900
TELEFAX: (610) 780-2679
TELEX: 79-0924
INFORMATION FOR SEQ ID NO. 94:
SEQUENCE CHARACTERISTICS:
```

```
Query Match
Best Local Similarity 100.0%, Prod No. 0.0012,
Matches 14, Conservative 0, Mismatches 0, Indels 0, Gaps 0

CY 1 SEQID=FFFFFSTK 14
| | | | | | | | | |
DB 21 SEQID=FFFFFSTK 34

RESULT 4
US 08 439 964-34
Sequence 94, Application US/08439964
Patent No. 5302243
GENERAL INFORMATION:
APPLICANT: BROWN, MICHAEL S.
APPLICANT: GOLDSTEIN, JOSEPH L.
APPLICANT: BEISS, YUVAL
APPLICANT: JAMES, GUY L.
TITLE OF INVENTION: METHODS FOR THE IDENTIFICATION OF PARNESYL
NUMBER OF SEQUENCES: 95
CORRESPONDENCE ADDRESS:
ADDRESS: 10000, WHITE & DRYER
STREET: P O BOX 4433
CITY: HOUSTON
STATE: TEXAS
COUNTRY: UNITED STATES OF AMERICA
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC DOS/MS DOS/ASCII
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08439964
FILING DATE: 27-APR-1995
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US/08439964
FILING DATE: 16-FEB-1993
CLASSIFICATION: 435
APPLICATION NUMBER: US/07922,611
FILING DATE: APPOINTED
CLASSIFICATION: 435
APPLICATION NUMBER: US/07922,611
FILING DATE: 20-NOV-1990
CLASSIFICATION: 435
APPLICATION NUMBER: US/07922,611
FILING DATE: 19-APR-1990 (APPOINTED)
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: PARKER, DAVID L.
REGISTRATION NUMBER: 32,165
REFERENCE/DOCKET NUMBER: US/07922,611/PAR
TELECOMMUNICATION INFORMATION:
TELEPHONE: (610) 418-3900
TELEFAX: (610) 780-2679
TELEX: 79-0924
INFORMATION FOR SEQ ID NO. 94:
SEQUENCE CHARACTERISTICS:
```


Query Match.
Best Local Similarity 100.0%, Prod No. 0.062, Indels 0, Gaps 0,
Matches 13; Conservative 0, Mismatches 0, Indels 0, Gaps 0,
SEQ ID NO:17; LENGTH: 16
5443956-17

Query Match.
Best Local Similarity 100.0%, Prod No. 0.062, Indels 0, Gaps 0,
Matches 13; Conservative 0, Mismatches 0, Indels 0, Gaps 0,

QY 1 SEDEHYFYSST 13
DB 4 SEDEHYFYSST 16

RESULT 8
US-08-985-337A-1
Sequence 1, Application US/08085337A
Patent No. 5932590
GENERAL INFORMATION:
APPLICANT: Ciccarone, Terrence M.
TITLE OF INVENTION: INHIBITORS OF PARNESYL-PROTEIN
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merck & Co., Inc.
STREET: P.O. Box 2000, 120 E. Lincoln Ave.
CITY: Rahway
STATE: NJ
COUNTRY: USA
ZIP: 07065-0900

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/985,337A
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/032,578
FILING DATE: 05-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Muthard, David A.
REGISTRATION NUMBER: 35,297
REFERENCE/DOCKET NUMBER: 19914Y
TELECOMMUNICATION INFORMATION:
TELEPHONE: 908-594-3903
TELEFAX: 908-594-4720
TELEX:
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-985-337A-1

Query Match.
Best Local Similarity 100.0%, Prod No. 0.062, Indels 0,
Matches 13; Conservative 0, Mismatches 0, Indels 0, Gaps 0,

QY 4 GPTTYYYSSTY 14
DB 1 GPTTYYYSSTY 11

RESULT 9

US-08-985-124A-1
Sequence 1, Application US/08085124A
Patent No. 5972966
GENERAL INFORMATION:
APPLICANT: deSolms, S. Jane
TITLE OF INVENTION: INHIBITORS OF PARNESYL-PROTEIN
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merck & Co., Inc.
STREET: P.O. Box 2000, 120 E. Lincoln Ave.
CITY: Rahway
STATE: NJ
COUNTRY: USA
ZIP: 07065-0900

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/985,124A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/032,428
FILING DATE: 05-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Muthard, David A.
REGISTRATION NUMBER: 35,297
REFERENCE/DOCKET NUMBER: 19933Y
TELECOMMUNICATION INFORMATION:
TELEPHONE: 908-594-3903
TELEFAX: 908-594-4720
TELEX:

INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-985-124A-1

Query Match 79.4%, Score 55; DP 2; Length 15;
Best Local Similarity 100.0%, Prod No. 0.062, Indels 0;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GPTTYYYSSTY 14
DB 1 GPTTYYYSSTY 11

RESULT 10

US-08-985-320A-1
Sequence 1, Application US/08085320A
Patent No. 5977134
GENERAL INFORMATION:
APPLICANT: Ciccarone, Terrence M.
APPLICANT: Halczenko, Wasyl
APPLICANT: Hutchinson, John H.
APPLICANT: Lumma, Jr., William C.
APPLICANT: Stokker, Gerald E.
APPLICANT: Stump, Craig A.
APPLICANT: Williams, Theresa M.
TITLE OF INVENTION: INHIBITORS OF PARNESYL-PROTEIN
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merck & Co., Inc.
STREET: P.O. Box 2000, 120 E. Lincoln Ave.
CITY: Rahway

Query Match 78.63; Score 55; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.062;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 GKKKKKKSKTK 14
DB 1 GKKKKKKSKTK 11

RESULT 12
US-09-195-578-13
; Sequence 13, Application US/09195578
; Patent No. 6054466
; GENERAL INFORMATION:
; APPLICANT: Ciccaccone, Terrence M.
; APPLICANT: deSolms, Jane S. J.
; APPLICANT: Merck & Co., Inc.
; TITLE OF INVENTION: INHIBITORS OF FARNESYL-PROTEIN
; FILE REFERENCE: 20121Y
; CURRENT APPLICATION NUMBER: US/09/195,578
; CURRENT FILING DATE: 1998-11-18
; EARLIER APPLICATION NUMBER: 60/067,552
; EARLIER FILING DATE: 1997-12-04
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 13
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homosapien
US-09-195-578-13

Query Match 78.63; Score 55; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.062;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 GKKKKKKSKTK 14
DB 1 GKKKKKKSKTK 11

RESULT 13
US-09-140-557-13
; Sequence 13, Application US/09140557A
; Patent No. 6103487
; GENERAL INFORMATION:
; APPLICANT: Merck & Co., Inc.
; APPLICANT: Barnett, Stanley F.
; APPLICANT: Heimbrock, David C.
; APPLICANT: Huber, Hans E.
; APPLICANT: Patrick, Denis R.
; TITLE OF INVENTION: A METHOD OF TREATING CANCER
; FILE REFERENCE: 20034Y
; CURRENT APPLICATION NUMBER: US/09/140,557A
; CURRENT FILING DATE: 1998-08-26
; EARLIER APPLICATION NUMBER: 60/057,342
; EARLIER FILING DATE: 1997-09-27
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 3.0

Query Match 78.63; Score 55; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.062;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 GKKKKKKSKTK 14
DB 1 GKKKKKKSKTK 11

RESULT 12
US-09-195-578-13
; Sequence 13, Application US/09195578
; Patent No. 6054466
; GENERAL INFORMATION:
; APPLICANT: Ciccaccone, Terrence M.
; APPLICANT: deSolms, Jane S. J.
; APPLICANT: Merck & Co., Inc.
; TITLE OF INVENTION: INHIBITORS OF FARNESYL-PROTEIN
; FILE REFERENCE: 20121Y
; CURRENT APPLICATION NUMBER: US/09/195,578
; CURRENT FILING DATE: 1998-11-18
; EARLIER APPLICATION NUMBER: 60/067,552
; EARLIER FILING DATE: 1997-12-04
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 13
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homosapien
US-09-195-578-13

Query Match 78.63; Score 55; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.062;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 GKKKKKKSKTK 14
DB 1 GKKKKKKSKTK 11

RESULT 13
US-09-140-557-13
; Sequence 13, Application US/09140557A
; Patent No. 6103487
; GENERAL INFORMATION:
; APPLICANT: Merck & Co., Inc.
; APPLICANT: Barnett, Stanley F.
; APPLICANT: Heimbrock, David C.
; APPLICANT: Huber, Hans E.
; APPLICANT: Patrick, Denis R.
; TITLE OF INVENTION: A METHOD OF TREATING CANCER
; FILE REFERENCE: 20034Y
; CURRENT APPLICATION NUMBER: US/09/140,557A
; CURRENT FILING DATE: 1998-08-26
; EARLIER APPLICATION NUMBER: 60/057,342
; EARLIER FILING DATE: 1997-09-27
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 3.0

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; SEQ ID NO 12
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthesized peptide substrate for
; OTHER INFORMATION: jernylgeranyl-protein transferase type I
US-09-140-557-13

```

```

; OTHER INFORMATION: synthesized peptide substrate for
; OTHER INFORMATION: jernylgeranyl-protein transferase type I
US-09-140-557-13

```

```

Query Match      78.6%; Score 55; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.062;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 4 GPKKKKKSKTK 14
   |||||
DB 1 GPKKKKKSKTK 11

```

RESULT 14

```
US-09-170-951-13
```

```

; Sequence 13, Application US/09164482A
; Patent No. 6103723
; GENERAL INFORMATION:
; APPLICANT: Bergman, Jeffrey M.
; APPLICANT: Binsmore, Christopher J.
; APPLICANT: Graham, Samuel L.
; APPLICANT: Merck & Co., Inc.
; TITLE OF INVENTION: INHIBITORS OF FARNESYL PROTEIN
; TITLE OF INVENTION: TRANSFERASE
; FILE REFERENCE: 19867Y
; CURRENT APPLICATION NUMBER: US/09/170,951
; CURRENT FILING DATE: 1998-10-13
; EARLIER APPLICATION NUMBER: 60/064,342
; EARLIER FILING DATE: 1997-10-17
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 13
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homosapien
US-09-170-951-13

```

```

Query Match      78.6%; Score 55; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.062;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 4 GPKKKKKSKTK 14
   |||||
DB 1 GPKKKKKSKTK 11

```

RESULT 15

```
US-09-164-482-13
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```

; Sequence 13, Application US/09164482A
; Patent No. 6127390
; GENERAL INFORMATION:
; APPLICANT: Merck & Co., Inc.
; APPLICANT: deSolms, S. Jane
; APPLICANT: Luma, William C.
; APPLICANT: Shaw, Anthony W.
; APPLICANT: Sisko, John T.
; APPLICANT: Tucker, Thomas J.
; TITLE OF INVENTION: INHIBITORS OF FARNYL PROTEIN TRANSFERASE
; FILE REFERENCE: 20025Y
; CURRENT APPLICATION NUMBER: US/09/164,482A
; CURRENT FILING DATE: 1998-10-01
; EARLIER APPLICATION NUMBER: 60/060,871
; EARLIER FILING DATE: 1997-10-02
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 13
; LENGTH: 15
; TYPE: PRT

```

```

; ORGANISM: Artificial Sequence

```

```

; FEATURE:
; OTHER INFORMATION: synthesized peptide substrate for
; OTHER INFORMATION: jernylgeranyl-protein transferase type I
US-09-164-482-13

```

```

Query Match      79.6%; Score 55; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.062;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 4 GPKKKKKSKTK 14
   |||||
DB 1 GPKKKKKSKTK 11

```

```

Search completed: March 3, 2003, 06:15:52
Job time: 10.878 secs

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transcription factor 1-pov protein, alternative splice form 1801 bp (fragment)
C:Species: Drosophila melanogaster
C:Title: A: 100 #seqname_revision: 10 #ext_change: 14 Nov 1994
C:Accession: A42089
F:Title: W. N. A. 100 #seqname_revision: 10 #ext_change: 14 Nov 1994
Cell: 64, 491-505, 1992
A:Title: Twin-51 protein, 51% identical difference in the 1001 bp (fragment)
A:Reference: A42089, MIM: 410466, PMID: 136784
A:Accession: A42089
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1116 nt
A:Note: Reference: A42089, MIM: 410466, PMID: 136784
A:Title: Sequence extracted from NCI library (NCBI)
A:Gene: Flybase: f000000
A:Cross reference: Flybase: FB000000
Query Match 20.5% Score 27 DB 2 Length 10
Best Local Similarity 55.0% Pval No. 6.7e-02
Matches 4, Conservative 2, Mismatches 2, Indels 0, Gaps 0
CY 2 GPPPPPPS 10
DB 1 GPPPPPPS 9
RESULT 4
S71300
1001 protein - Parametrium tetraurelia (fragment)
C:Species: Parametrium tetraurelia
C:Title: M. 1001 #seqname_revision: 10 #ext_change: 14 Nov 1994
C:Accession: S71300
R:Madhavi, G., Klotz, C., Le Goff, J.P., Beisson, J.
Eur. J. Biochem. 234, 121-128, 1996
A:Title: Characterization of dentin genes in Parametrium.
A:Reference: A42089, MIM: 410466, PMID: 136784
A:Accession: S71300
A:Molecule type: Protein
A:Residues: 115 <MAD>
A:Experimental source: strain 34-2
C:Genetic code: 3505
Query Match 31.1% Score 20 DB 2 Length 10
Best Local Similarity 39.6% Pval No. 1.4e-01
Matches 4, Conservative 1, Mismatches 3, Indels 0, Gaps 0
CY 1 GPPPPPPPPPPPP 10
DB 2 GPPPPPPPPPPPP 15
RESULT 5
G45681
1001 protein - Parametrium tetraurelia (fragment)
C:Species: parametrium tetraurelia
C:Title: M. 1001 #seqname_revision: 10 #ext_change: 14 Nov 1994
C:Accession: G45681
R:Selick, H.E., Storno, G.D., Dysan, R.L., Alberts, B.M.
Cell. 67, 2305-2316, 1993
A:Title: Analysis of five presynaptic protein-coding sequences clustered between the protein-coding genes of the parametrium.
A:Reference number: A45681, MIM: 410466, PMID: 938213
A:Accession: G45681
A:Status: Preliminary; not compared with conceptual translation
A:Molecule type: nucleic acid
A:Residues: 116 nt
A:Note: Sequence extracted from NCI library (NCBI)
Query Match 31.1% Score 20 DB 2 Length 10
Best Local Similarity 39.6% Pval No. 1.4e-01
Matches 4, Conservative 1, Mismatches 3, Indels 0, Gaps 0

```

```

CY 4 GPPPPPPS 10
DB 4 GPPPPPPS 15
RESULT 6
S70716
1001 protein - Parametrium tetraurelia (fragment)
C:Species: parametrium tetraurelia
C:Title: M. 1001 #seqname_revision: 10 #ext_change: 14 Nov 1994
C:Accession: S70716
R:Selick, H.E., Storno, G.D., Dysan, R.L., Alberts, B.M.
Cell. 67, 2305-2316, 1993
A:Title: Analysis of five presynaptic protein-coding sequences clustered between the protein-coding genes of the parametrium.
A:Reference number: A45681, MIM: 410466, PMID: 938213
A:Accession: S70716
A:Status: Preliminary; not compared with conceptual translation
A:Molecule type: nucleic acid
A:Residues: 116 nt
A:Note: Sequence extracted from NCI library (NCBI)
Query Match 31.1% Score 20 DB 2 Length 10
Best Local Similarity 39.6% Pval No. 1.4e-01
Matches 4, Conservative 1, Mismatches 3, Indels 0, Gaps 0
CY 3 GPPPPPPPPPPPP 13
DB 3 GPPPPPPPPPPPP 13
RESULT 7
A28719
Thymic humoral factor gamma-2 - bovine (fragment)
C:Species: Bos taurus (cattle)
C:Title: 10-Sep-1989 #seqname_revision: 10 #ext_change: 14 Nov 1994
C:Accession: A28719
R:Burstein, Y., Buchner, V., Pecht, M., Trainin, N.
Biochemistry 17, 4022-4021, 1989
A:Title: Thymic humoral factor gamma-2: purification and amino acid sequence of an immunoreactive peptide.
A:Reference number: A28719, MIM: 410466, PMID: 136784
A:Accession: A28719
A:Molecule type: protein
A:Residues: 1-8 <BUR>
Query Match 26.9% Score 24 DB 2 Length 8
Best Local Similarity 100.0% Pval No. 2.8e-05
Matches 4, Conservative 0, Mismatches 0, Indels 0, Gaps 0
CY 1 GPP 4
DB 3 GPP 6
RESULT 8
S36893
1001 protein - Parametrium tetraurelia (fragment)
C:Species: Parametrium tetraurelia
C:Title: M. 1001 #seqname_revision: 10 #ext_change: 14 Nov 1994
C:Accession: S36893
R:Chen, H., Kimura, M., Higashi, Y., Yamada, T.
FEBS Lett. 331, 9-14, 1993
A:Title: Isolation and amino acid sequence of the parametrium protein-coding gene.
A:Reference number: S36893, MIM: 410466, PMID: 136784
A:Accession: S36893

```


Query Match 24: DB 21, Score 21; 18 21; Length 14;
Best Local Similarity 50.0%; Pred. No. 64-03;
Matches 1; Mismatches 0; Gaps 0;
C:Accession: H64008
R:Flotischmann, E.D.; Adams, M.D.; White, C.; Clayton, P.A.; Fiksdal, E.H.; R. Tharion,
D.M.; Brandon, R.C.; Pine, L.D.; Fritzman, J.L.; Fiksdal, A.; Bailey, J.W.; Westman,
Science 269, 490-510, 1998
A:Authors: Gnehm, C.B.; McDonald, L.A.; Small, K.V.; Fraser, J.M.; Smith, H.; Westman,
A:Title: Whole-genome random sequencing and assembly of Haemophilus influenzae HI
A:Reference number: A64000; MIM:235359.1; IM:00044.80
A:Accession: H64008
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-14 <TIGR>
A:Cross-references: GB:002131; GB:044224; MIM:235359.1; IM:00044.80; IM:00044.80

Query Match 25: DB 21, Score 21; 18 21; Length 14;
Best Local Similarity 50.0%; Pred. No. 64-03;
Matches 5; Conservative 0; Mismatches 0; Gaps 0;
QY 4 KKKKKKSPSK 13
DB 2 PKYKPKPKPK 11

Query Match 26: DB 21, Score 21; 18 21; Length 14;
Best Local Similarity 50.0%; Pred. No. 64-03;
Matches 1; Mismatches 0; Gaps 0;
C:Accession: P20040
R:Dombardi, V.; Willis, A.C.; Vereb, J.; Johnson, L.N.
Comp. Biochem. Physiol. B 91, 217-221, 1998
A:Title: The sequence around the phosphorylation site of the porcine heart type 1b glycogen
A:Reference number: P20040; MIM:289165.1; IM:00044.80
A:Accession: P20040
A:Molecule type: protein
A:Residues: 1-14 <DM>
A:Experimental source: heart
A:Keywords: allosteric regulation; cardiac muscle; glycogen metabolism; glycolysis; muscle
P:Binding site: phosphate 300; phosphate 450; phosphate 450; phosphate 450

Query Match 27: DB 21, Score 21; 18 21; Length 14;
Best Local Similarity 42.9%; Pred. No. 64-03;
Matches 3; Conservative 0; Mismatches 1; Gaps 0;
QY 1 DGPKKK 7
DB 2 DGPKKK 8

Query Match 28: DB 21, Score 21; 18 21; Length 14;
Best Local Similarity 50.0%; Pred. No. 64-03;
Matches 1; Mismatches 0; Gaps 0;
C:Accession: P20118
R:Sukhomlinov, B.F.; Konechenko, S.V.
Mol. Biol. (Mosk.) 5, 415-418, 1971
A:Title: Study on N-terminal sequence of the haemoglobin of the haemoglobin of the
A:Reference number: P20117
A:Accession: P20118
A:Molecule type: protein
A:Residues: 1-15 <SU>
A:Superfamily: globin; globin homology
C:Keywords: blood; erythrocyte; hemoglobin; hemoglobin; hemoglobin; hemoglobin

Query Match 29: DB 21, Score 21; 18 21; Length 14;
Best Local Similarity 41.7%; Pred. No. 64-03;
Matches 5; Conservative 1; Mismatches 6; Gaps 0;
QY 1 DGPKKK 7
DB 2 DGPKKK 8

Query Match 11: DB 21, Score 21; 18 21; Length 14;
Best Local Similarity 50.0%; Pred. No. 64-03;
Matches 1; Mismatches 0; Gaps 0;
C:Accession: H64008
R:Flotischmann, E.D.; Adams, M.D.; White, C.; Clayton, P.A.; Fiksdal, E.H.; R. Tharion,
D.M.; Brandon, R.C.; Pine, L.D.; Fritzman, J.L.; Fiksdal, A.; Bailey, J.W.; Westman,
Science 269, 490-510, 1998
A:Authors: Gnehm, C.B.; McDonald, L.A.; Small, K.V.; Fraser, J.M.; Smith, H.; Westman,
A:Title: Whole-genome random sequencing and assembly of Haemophilus influenzae HI
A:Reference number: A64000; MIM:235359.1; IM:00044.80
A:Accession: H64008
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-14 <TIGR>
A:Cross-references: GB:002131; GB:044224; MIM:235359.1; IM:00044.80; IM:00044.80

Query Match 12: DB 21, Score 21; 18 21; Length 14;
Best Local Similarity 50.0%; Pred. No. 64-03;
Matches 5; Conservative 0; Mismatches 0; Gaps 0;
QY 4 KKKKKKSPSK 13
DB 2 PKYKPKPKPK 11

Query Match 13: DB 21, Score 21; 18 21; Length 14;
Best Local Similarity 42.9%; Pred. No. 64-03;
Matches 3; Conservative 0; Mismatches 1; Gaps 0;
QY 1 DGPKKK 7
DB 2 DGPKKK 8

Query Match 14: DB 21, Score 21; 18 21; Length 14;
Best Local Similarity 50.0%; Pred. No. 64-03;
Matches 1; Mismatches 0; Gaps 0;
C:Accession: P20118
R:Sukhomlinov, B.F.; Konechenko, S.V.
Mol. Biol. (Mosk.) 5, 415-418, 1971
A:Title: Study on N-terminal sequence of the haemoglobin of the haemoglobin of the
A:Reference number: P20117
A:Accession: P20118
A:Molecule type: protein
A:Residues: 1-15 <SU>
A:Superfamily: globin; globin homology
C:Keywords: blood; erythrocyte; hemoglobin; hemoglobin; hemoglobin; hemoglobin

Query Match 15: DB 21, Score 21; 18 21; Length 14;
Best Local Similarity 41.7%; Pred. No. 64-03;
Matches 5; Conservative 1; Mismatches 6; Gaps 0;
QY 1 DGPKKK 7
DB 2 DGPKKK 8

QY 5 KKKKSPKSSG 16
 : : : :
 Db 4 KKKKSPKSSG 15

RESULT 14

A27803
 Cyslin light chain, smooth muscle - turkey (fragment)
 C:Species: Meleagris gallopavo (common turkey)
 C:Date: 05-Jun-1994 #sequence_revision 05-Jun-1994 #text_change 29-Sep-1999
 C:Accession: A27803
 R:Receptor: A.R.; Robinson, E.A.; Appella, E.; Sellers, J.R.
 J. Biol. Chem. 262, 7613-7617, 1987
 A:Title: Sequence of the sites phosphorylated by protein kinase C in the smooth muscle m
 A:Reference number: A27803; MUID:9722380; PMID:3584131
 A:Accession: A27803
 A:Molecule type: protein
 A:Residues: 1-16 <BN>
 C:Superfamily: calmodulin, calmodulin-regulat homology
 C:Keywords: EF hand; muscle; smooth muscle

Query Match 25.33, Score 21, DB 2, Length 16;
 Best Local Similarity 44.4%; Pred. No. 6.7e+03;
 Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 5 KKKKSPK 13
 : : : :
 Db 8 KKKKSPK 15

RESULT 15

PH0137
 T-cell receptor beta chain V-D-J region MS20 - human (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 23-Nov-1991 #sequence_revision 02-Nov-1991 #text_change 10-May-1997
 C:Accession: PH0137
 R:Receptor: F.; Howell, M.D.; Karamanlidis, D.; Flanagan, M.; Rickett, J.; Briscoff, S.; In
 J. Exp. Med. 173, 19-24, 1991
 A:Title: A myelin basic protein peptide is recognized by cytotoxic T cells in the contex
 A:Reference number: PH0137; PMID:5106643; PMID:1702137
 A:Accession: PH0137
 A:Molecule type: mRNA
 A:Residues: 1-16 <MAR>
 C:Keywords: T-cell receptor

Query Match 25.33, Score 21, DB 2, Length 16;
 Best Local Similarity 66.7%; Pred. No. 6.7e+03;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 7 KKKSPS 12
 : : : :
 Db 7 RKDPS 12

Search completed: March 3, 2003, 06:46:26
 Job time : 14.6667 secs

34 17 20.5 16 1 RPL_VIOL1
35 17 20.5 16 1 YMKR_PSEPO
36 16 19.3 8 1 R57_MY11
37 16 19.3 9 1 PAR3_CALVO
38 16 19.3 9 1 SAMP_MISCA
39 16 19.3 9 1 THY1_FTS
40 16 19.3 11 1 TKNA_PANP1
41 16 19.3 12 1 TKNI_KASMA
42 16 19.3 13 1 BRK_FARD1
43 16 19.3 14 1 HV14_FTS
44 16 19.3 15 1 FIRA_ANAPL
45 16 19.3 15 1 MK1_PALUP

34 17 20.5 16 1 RPL_VIOL1
35 17 20.5 16 1 YMKR_PSEPO
36 16 19.3 8 1 R57_MY11
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38 16 19.3 9 1 SAMP_MISCA
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44 16 19.3 15 1 FIRA_ANAPL
45 16 19.3 15 1 MK1_PALUP

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35 17 20.5 16 1 YMKR_PSEPO
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40 16 19.3 11 1 TKNA_PANP1
41 16 19.3 12 1 TKNI_KASMA
42 16 19.3 13 1 BRK_FARD1
43 16 19.3 14 1 HV14_FTS
44 16 19.3 15 1 FIRA_ANAPL
45 16 19.3 15 1 MK1_PALUP

34 17 20.5 16 1 RPL_VIOL1
35 17 20.5 16 1 YMKR_PSEPO
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43 16 19.3 14 1 HV14_FTS
44 16 19.3 15 1 FIRA_ANAPL
45 16 19.3 15 1 MK1_PALUP

34 17 20.5 16 1 RPL_VIOL1
35 17 20.5 16 1 YMKR_PSEPO
36 16 19.3 8 1 R57_MY11
37 16 19.3 9 1 PAR3_CALVO
38 16 19.3 9 1 SAMP_MISCA
39 16 19.3 9 1 THY1_FTS
40 16 19.3 11 1 TKNA_PANP1
41 16 19.3 12 1 TKNI_KASMA
42 16 19.3 13 1 BRK_FARD1
43 16 19.3 14 1 HV14_FTS
44 16 19.3 15 1 FIRA_ANAPL
45 16 19.3 15 1 MK1_PALUP

```

GN RPSS OR RPS19.
OS Cloner ribosomal protein, rRNA-binding.
OC Bacteria; Firmicutes; Mollicutes; Achaeplastmatales;
OC Achaeplastmatales; Phytoplasmata.
OX NCBI_TaxID=35776;
RN [1]
RP SEQUENCE FROM N.A.
FX MEDLINE 1465244-5254(1994).
RA Gunderson D.E., Lee I.M., Rehner S.A., Davis R.E., Kingbury D.T.
RT "Phylogeny of mycoplasma-like organisms (phytoplasmata): a basis for
PT their classification".
PL J. Bacteriol. 176(12):44-5254(1994).
CC 1- PUNTING: 157111.03.114X: A. C. WILKIN WITH 114 THAT RINDS STRONGLY
CC TO THE 16S RIBOSOMAL RNA (BY SIMILARITY).
CC 1- SIMILARITY: BELONGS TO THE SIB FAMILY OF RIBOSOMAL PROTEINS.
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CC or send an email to license@ebi.ac.uk.
CC
CC EMBL: L27027; AAA03944.1;
DE Bacteria; Firmicutes; Mollicutes; Achaeplastmatales;
FX PROSITE: PS00123; RIBOSOMAL_S19; PARTIAL.
KW Ribosomal protein, rRNA-binding.
FT NON-TER 1
SC SEQUENCE 14 AA; 1642 MW; 20C478EB9FFFE48P CRC64;

Query Match 31.91; Score 25; DR 1; Length 14;
Best local similarity 31.91; Pct 100; Mismatches 0;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Q/ 2 GPPPPPPY 9
D/ 7 GGRKKKK 14

RESULT 3
RPS19 LOWEP
ID RPS19 LOWEP STANDARD; PRT; 14 AA.
AC Q48879;
DT 10-MAY-2000 (rel 30, last sequence update)
DT 10-MAY-2000 (rel 30, last annotation update)
DE 30S ribosomal protein S19 (fragment).
GN RPS19 LOWEP.
OS Loofah witches'-broom phytoplasmata.
OC Bacteria; Firmicutes; Mollicutes; Achaeplastmatales;
OC Achaeplastmatales; Phytoplasmata.
OX NCBI_TaxID=35776;
RN [1]
RP SEQUENCE FROM N.A.
FX MEDLINE 1465244-5254(1994).
RA Gunderson D.E., Lee I.M., Rehner S.A., Davis R.E., Kingbury D.T.
RT "Phylogeny of mycoplasma-like organisms (phytoplasmata): a basis for
PT their classification".
PL J. Bacteriol. 176(12):44-5254(1994).
CC 1- PUNTING: 157111.03.114X: A. C. WILKIN WITH 114 THAT RINDS STRONGLY
CC TO THE 16S RIBOSOMAL RNA (BY SIMILARITY).
CC 1- SIMILARITY: BELONGS TO THE SIB FAMILY OF RIBOSOMAL PROTEINS.
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CC or send an email to license@ebi.ac.uk.
CC
CC EMBL: L27027; AAA03944.1;
DE Bacteria; Firmicutes; Mollicutes; Achaeplastmatales;
FX PROSITE: PS00123; RIBOSOMAL_S19; PARTIAL.
KW Ribosomal protein, rRNA-binding.
FT NON-TER 1
SC SEQUENCE 14 AA; 1642 MW; 20C478EB9FFFE48P CRC64;

Query Match 28.91; Score 24; DR 1; Length 14;
Best local similarity 28.91; Pct 100; Mismatches 0;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Q/ 2 GPPPPPPPPSPK 13
D/ 7 GPPPPPPPPPP 13

RESULT 5
RPS19 PRUAP
ID RPS19 PRUAP STANDARD; PRT; 14 AA.
AC Q44160;
DT 10-MAY-2000 (rel 30, last sequence update)
DT 10-MAY-2000 (rel 30, last annotation update)
DE 30S ribosomal protein S19 (fragment).
GN RPS19 PRUAP.
OS Finus almeriaca phytoplasmata.

```



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CC C + 2 H2O/O
FW Oxidoreductase, Matriculation
FT NON-TER 10 10
SQ SEQUENCE 10 AA, 1210 MW, 27052/7743322 CPO04;

Query Match 24.1%, Score 20, DB 1, Length 10,
Best Local Similarity 50.0%, Field No. 17, Indels 0,
Matches 3, Mismatches 0, Conservative 0, Gaps 0,

CY - PPTPTT 10
|||
DB 3 QKPTPT 8

RESULT 2
RPOC_MYCGA STANFORD, PPT, 13 AA,
AC P4716;
DI 01-FEB-1996 (Rel 33, Created)
ET 01-FEB-1996 (Rel 33, Last sequence update)
DT 16-OCT-2000 (Rel 40, Last annotation update)
DE RNA directed RNA polymerase beta' chain (EF 27766) (Transcriptase
DE beta' chain) (RNA polymerase beta' subunit) (Fragment)
GN RPOC
OS Mycoplasma Gallisepticum
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma
CY NCBI_TaxID:107
RN [1]
RP SEQUENCE FROM N.A.
R1 STAFF AGOSVAT F.
RA Rebeaulashvili R S;
RL Submitted (XXY 1000) to the EMBL/GenBank/CCP databases
CC 1. FUNCTION: RNA DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION
CC OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
CC SUBSTRATES
CC 1-1 CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
CC {RNA}(N)
CC 1. SUBMIT: THE ENZYME CONSISTS OF THE SIGMA CHAIN AND THE CORE
CC ENZYME WHICH IS COMPOSED OF 2 ALPHA CHAINS, 1 BETA CHAIN, AND 1
CC BETA' CHAIN.
CC 1-1 SIMILARITY: BELONGS TO THE RNA POLYMERASE BETA' CHAIN FAMILY.
CC
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CC
CC EMBL: L39403; AAB40952.1;
CC Transcription: RNA directed RNA polymerase, Transcription.
FT NON-TER 11 11
SQ SEQUENCE 13 AA, 1430 MW, 482777496433 CPO44;

Query Match 24.1%, Score 20, DB 1, Length 10,
Best Local Similarity 50.0%, Field No. 20, Indels 0,
Matches 4, Conservative 0, Mismatches 0, Indels 0, Gaps 0,

CY 1 PPTPTT 8
|||
DB 1 PPTPTT 11

RESULT 10
RS19_PPWP RP STANFORD, PPT, 14 AA
AC Q2000;
DI 30-MAY-2000 (Rel 39, Last sequence update)
DT 30-MAY-2000 (Rel 39, Last annotation update)
DE 30S ribosomal protein S19 (Fragment).
DE 30S ribosomal protein S19 (Fragment).

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AC P12509;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE TAT protein (Transactivating regulatory protein) (Fragment)
GN TAT
OS Human immunodeficiency virus type 1 (HIV-1)
OC Viruses; Retroviridae; Lentivirus.
OX NCBI TaxID:11795;
RN [1]
RP SEQUENCE FROM N.A.
RA Hahn B.H., Shaw G.M., Taylor M.E., Redfield R.B., Markham P.D.,
RA Gallo R.C., Weng S.G., Parks W.F., Parks E.S., Parks W.F.,
RA Genetic variation in HIV-1/HIV/LAV over time in patients with AIDS or
RT at risk for AIDS."
RL Sequence 214-913-37 (1998).
CC : FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE
CC TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND
CC ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR
CC PROMOTER.
CC -!- SUBUNIT: BINDS CYCLIN T1 (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Nucleus; RNA Binding; Nuclear protein;
CC : MISCELLANEOUS: LOCATES WITH WM1, WM2, AND WM3 WERE OBTAINED FROM
CC BLOOD SAMPLES SEQUENTIALLY TAKEN FROM A TWO YEAR OLD HAITIAN WHO
CC WAS PERINATALLY INFECTED BY HER MOTHER.
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CC or send an email to license@isb-sib.ch).
CC EMBL: M12507; AAB12991.1;
DR HIV; M12507; TATSWM2.
KW AIDS
KW Transcription regulation, Activation, RNA-Binding, Nuclear protein;
FT NON_TER 1 146 MW: 370C737BF8F67AA8 CR664;
SQ SEQUENCE 14 AA: 146 MW: 370C737BF8F67AA8 CR664;
Query Match 22.9%; Score 19; DB 1; Length 14;
Best Local Similarity 75.0%; Pred. NO. 3.3e+03;
Matcher 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 2 GPKK 5
DB 11 GPKK 14
RESULT 15
TAT_HV128
ID TAT_HV128 STANDARD; PRT; 14 AA.
AC P12511;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE TAT protein (Transactivating regulatory protein) (Fragment).
GN TAT.
OS Human immunodeficiency virus type 1 (2.94 isolate) (HIV-1).
OC Viruses; Retroviridae; Lentivirus.
OX NCBI TaxID:11795;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE 88281278; PubMed-3395517;
RA Hahn B.H., Shaw G.M., Taylor M.E., Redfield R.B., Markham P.D.,
RA Gallo R.C.,
RA "Nucleotide sequence analysis of the env gene of a new Haitian
PT isolate of HIV-1."
PL AIDS Res. Hum. Retroviruses 4:165-173(1988).
CC -!- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE
CC TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND

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CC ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR
CC PROMOTER.
CC -!- SUBUNIT: BINDS CYCLIN T1 (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Nucleus; RNA Binding; Nuclear protein;
CC : MISCELLANEOUS: THE 2.94 ISOLATE WAS TAKEN FROM A TWO YEAR OLD
CC ZAIRIAN MALE.
CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).
CC EMBL: J03653; AAA44685.1;
DR HIV; J03653; TATSWM1.
KW AIDS
KW Transcription regulation, Activation, RNA-Binding, Nuclear protein;
FT NON_TER 1 1453 MW: 370C737BF8F67AA8 CR664;
SQ SEQUENCE 14 AA: 1453 MW: 370C737BF8F67AA8 CR664;
Query Match 22.9%; Score 19; DB 1; Length 14;
Best Local Similarity 75.0%; Pred. NO. 3.3e+03;
Matcher 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 2 GPKK 5
DB 11 GPKK 14
Search completed March 3, 2003, 06:42:07
File: us-09-214-913-37

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File version: 1.00 - 2003-07-01

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Figure 1



















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Figure 1. The effect of the number of trials on the number of correct responses. The number of correct responses was plotted against the number of trials for each condition. The number of correct responses increased with the number of trials for all conditions. The number of correct responses was highest for the condition with the highest number of trials (10 trials) and lowest for the condition with the lowest number of trials (2 trials).

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1. The first part of the document is a list of names and their corresponding addresses. The names are listed in a column on the left, and the addresses are listed in a column on the right. The names are: John Doe, Jane Smith, and Bob Johnson. The addresses are: 123 Main St, 456 Elm St, and 789 Oak St.

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CR 997
CR 998
CR 999
CR 1000

Q94623 manduca sov

Sample	Monomer	Yield (%)	η_{inh} (dL/g)	M_n (g/mol)	M_w (g/mol)	M_w/M_n
1	Styrene	95	0.45	12,500	18,000	1.44
2	Styrene	95	0.45	12,500	18,000	1.44
3	Styrene	95	0.45	12,500	18,000	1.44
4	Styrene	95	0.45	12,500	18,000	1.44
5	Styrene	95	0.45	12,500	18,000	1.44
6	Styrene	95	0.45	12,500	18,000	1.44
7	Styrene	95	0.45	12,500	18,000	1.44
8	Styrene	95	0.45	12,500	18,000	1.44
9	Styrene	95	0.45	12,500	18,000	1.44
10	Styrene	95	0.45	12,500	18,000	1.44
11	Styrene	95	0.45	12,500	18,000	1.44
12	Styrene	95	0.45	12,500	18,000	1.44
13	Styrene	95	0.45	12,500	18,000	1.44
14	Styrene	95	0.45	12,500	18,000	1.44
15	Styrene	95	0.45	12,500	18,000	1.44
16	Styrene	95	0.45	12,500	18,000	1.44
17	Styrene	95	0.45	12,500	18,000	1.44
18	Styrene	95	0.45	12,500	18,000	1.44
19	Styrene	95	0.45	12,500	18,000	1.44
20	Styrene	95	0.45	12,500	18,000	1.44
21	Styrene	95	0.45	12,500	18,000	1.44
22	Styrene	95	0.45	12,500	18,000	1.44
23	Styrene	95	0.45	12,500	18,000	1.44
24	Styrene	95	0.45	12,500	18,000	1.44
25	Styrene	95	0.45	12,500	18,000	1.44
26	Styrene	95	0.45	12,500	18,000	1.44
27	Styrene	95	0.45	12,500	18,000	1.44
28	Styrene	95	0.45	12,500	18,000	1.44
29	Styrene	95	0.45	12,500	18,000	1.44
30	Styrene	95	0.45	12,500	18,000	1.44
31	Styrene	95	0.45	12,500	18,000	1.44
32	Styrene	95	0.45	12,500	18,000	1.44
33	Styrene	95	0.45	12,500	18,000	1.44
34	Styrene	95	0.45	12,500	18,000	1.44
35	Styrene	95	0.45	12,500	18,000	1.44
36	Styrene	95	0.45	12,500	18,000	1.44
37	Styrene	95	0.45	12,500	18,000	1.44
38	Styrene	95	0.45	12,500	18,000	1.44
39	Styrene	95	0.45	12,500	18,000	1.44
40	Styrene	95	0.45	12,500	18,000	1.44
41	Styrene	95	0.45	12,500	18,000	1.44
42	Styrene	95	0.45	12,500	18,000	1.44
43	Styrene	95	0.45	12,500	18,000	1.44
44	Styrene	95	0.45	12,500	18,000	1.44
45	Styrene	95	0.45	12,500	18,000	1.44
46	Styrene	95	0.45	12,500	18,000	1.44
47	Styrene	95	0.45	12,500	18,000	1.44
48	Styrene	95	0.45	12,500	18,000	1.44
49	Styrene	95	0.45	12,500	18,000	1.44
50	Styrene	95	0.45	12,500	18,000	1.44
51	Styrene	95	0.45	12,500	18,000	1.44
52	Styrene	95	0.45	12,500	18,000	1.44
53	Styrene	95	0.45	12,50		

[illegible]

Q950w9 polymaviru

Matches 4; Conservative 1; Mismatches 0; Gaps 0

QY 11 PKSSG 16
|||

Db 3 PKSSG 8

RESULT 11

Q900X9
ID Q900X9 PRELIMINARY; PRT; 10 AA.
AC Q900X9
DT 01-MAY-2000 (TREMblrel. 13, Created)
DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
DE Large T antigen (Fragment).
OS Polymavirus JC.
OC Viruses, dsRNA viruses, ss RNA stage, Polyomaviridae; Polyomavirus.
CX NCBI_TaxID=10632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BCN16;
PX MCELINER2097544, PubMed 10612530;
FA Hoffill-Mas S., Pina S., Girones R.,
RT "Documenting the epidemiologic patterns of polyomaviruses in human
populations by studying their presence in urban sewage."
PI Afl19347, Microbiol. 13, 144 (2000).
DR EMBL, Afl19347; AAF24100.1;
FT NON TER 1
SQ SEQUENCE 10 AA; 1167 MW; 4256A07771A32263 CRC64;

Query Match 27.71; Score 23; DB 12; Length 10;
Best Local Similarity 55.63; Pred No. 2.9e+03;
Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0

QY 5 KYYVTPSPY 13
|||

Db 2 KYYVTPSPY 10

RESULT 12

Q900X5
ID Q900X5 PRELIMINARY; PRT; 10 AA.
AC Q900X5
DT 01-MAY-2000 (TREMblrel. 13, Created)
DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
DE Large T antigen (Fragment).
OS Polymavirus JC.
OC Viruses, dsRNA viruses, ss RNA stage, Polyomaviridae; Polyomavirus.
CX NCBI_TaxID=10632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BCN16;
PX MCELINER2097544, PubMed 10612530;
FA Hoffill-Mas S., Pina S., Girones R.,
RT "Documenting the epidemiologic patterns of polyomaviruses in human
populations by studying their presence in urban sewage."
PI Afl19347, Microbiol. 13, 144 (2000).
DR EMBL, Afl19347; AAF24100.1;
FT NON TER 1
SQ SEQUENCE 10 AA; 1167 MW; 4256A07771A32263 CRC64;

Query Match 27.71; Score 23; DB 12; Length 10;
Best Local Similarity 55.63; Pred No. 2.9e+03;
Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0

QY 5 KYYVTPSPY 13
|||

Db 2 KYYVTPSPY 10

Matches 4; Conservative 1; Mismatches 0; Gaps 0

QY 11 PKSSG 16
|||

Db 3 PKSSG 8

RESULT 11

Q900X9
ID Q900X9 PRELIMINARY; PRT; 10 AA.
AC Q900X9
DT 01-MAY-2000 (TREMblrel. 13, Created)
DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
DE Large T antigen (Fragment).
OS Polymavirus JC.
OC Viruses, dsRNA viruses, ss RNA stage, Polyomaviridae; Polyomavirus.
CX NCBI_TaxID=10632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BCN16;
PX MCELINER2097544, PubMed 10612530;
FA Hoffill-Mas S., Pina S., Girones R.,
RT "Documenting the epidemiologic patterns of polyomaviruses in human
populations by studying their presence in urban sewage."
PI Afl19347, Microbiol. 13, 144 (2000).
DR EMBL, Afl19347; AAF24100.1;
FT NON TER 1
SQ SEQUENCE 10 AA; 1167 MW; 4256A07771A32263 CRC64;

Query Match 27.71; Score 23; DB 12; Length 10;
Best Local Similarity 55.63; Pred No. 2.9e+03;
Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0

QY 5 KYYVTPSPY 13
|||

Db 2 KYYVTPSPY 10

RESULT 12

Q900X5
ID Q900X5 PRELIMINARY; PRT; 10 AA.
AC Q900X5
DT 01-MAY-2000 (TREMblrel. 13, Created)
DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
DE Large T antigen (Fragment).
OS Polymavirus JC.
OC Viruses, dsRNA viruses, ss RNA stage, Polyomaviridae; Polyomavirus.
CX NCBI_TaxID=10632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BCN16;
PX MCELINER2097544, PubMed 10612530;
FA Hoffill-Mas S., Pina S., Girones R.,
RT "Documenting the epidemiologic patterns of polyomaviruses in human
populations by studying their presence in urban sewage."
PI Afl19347, Microbiol. 13, 144 (2000).
DR EMBL, Afl19347; AAF24100.1;
FT NON TER 1
SQ SEQUENCE 10 AA; 1167 MW; 4256A07771A32263 CRC64;

Query Match 27.71; Score 23; DB 12; Length 10;
Best Local Similarity 55.63; Pred No. 2.9e+03;
Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0

QY 5 KYYVTPSPY 13
|||

Db 2 KYYVTPSPY 10

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11 40.5 48.8 15 7 AAB60118
12 40 48.2 15 18 AAW23484
13 40 48.2 15 20 AAY34347
14 40 48.2 15 21 AAY57445
15 39 47.0 9 21 AAB26621
16 39 47.0 12 23 ABB74771
17 39 47.0 13 21 AAY58859
18 39 47.0 14 17 AAW24466
19 39 47.0 15 20 AAY43338
20 39 47.0 15 20 AAY77777
21 39 47.0 15 20 AAY29463
22 39 47.0 15 20 AAY18334
23 39 47.0 15 20 AAY18334
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44 39 47.0 15 20 AAY18334
45 39 47.0 15 20 AAY18334

ALIGNMENTS

RESULT 1
AAW45878
15 AAW45878 standard; peptide; 16 AA.
AC AAW45878;
XX 30-CTC-1399 (first entry)
XX Peptide membrane binding element.
XX Membrane binding element, thrombotic disease, inflammation;
XX Complement related disease, soluble peptide.
OS Synthetic.
IN W00000454-1.
XX 22-JAN-1998.
XX 08-JUL-1997; 97WO-EP03715.
XX 15-JUL-1996; 96CP-0014871.
XX (ADPR-) ADPROTECH PLC.
XX Dodd I, Mossakowski DEI, Smith RAG;
XX WPI; 1998-110534/10.
XX Derivatives of soluble poly-peptides bonded to low affinity/
XX membrane binding groups for tracking complement related and
XX thrombotic diseases, following intravascular localization at cellular
XX membranes

of results predicted by chance to have a
equal to the score of the result being predicted,
basis of the total score distribution.

SUMMARIES

SP	ID	Description
1	AAW45878	Peptide membrane b
2	AAW45878	Membrane binding e
3	AAW45878	Antibacterial memb
4	AAW45878	Peptide membrane b
5	AAW45878	Membrane binding e
6	AAW45878	Antibacterial memb
7	AAW45878	Peptide membrane b
8	AAW45878	Antibacterial memb
9	AAW45878	Peptide membrane b
10	AAW45878	Membrane binding e

Best Local Similarity 100.0%; Prod No. 6 to 05;
Matches 10, Conservation 0, Mismatches 0, Gaps 0

CY 1 DGPFFRFFRFFSSSS 15
||||| ||||| |||||
DB 1 DGPFFRFFRFFSSSS 15

RESULT 6
ABB81240
ID ABB81240 standard; peptide; 16 AA.
XX
AC ABB81240;
XX
CT 20-AUG-2002 (first entry)
XX
DE Antibacterial membrane binding peptide SEQ ID NO.7.
XX
KW Antibacterial, glycopeptide, peptidic membrane associating element,
XX Penicillin, infection, macrolide, peptidoglycan biosynthesis inhibition,
XX antibiotic.
XX
OS Synthetic.
XX
PN WO9902454 A1.
XX
PD 10-MAY-2002.
XX
PE 02 NOV 2001; 2001WG 0604967.
XX
PF 03 NOV 2001; 2001WB 0604967.
XX
PG (OYCA-) UNIV CAMBRIDGE TECH SERVICES LTD.
XX
PA (ADGK-) APPROTECH LTD.
XX
PI Cooper MA, Betley JR;
XX
PP WPI, 2002 471499/10.
XX
PT Antibacterial compound, useful for the treatment of a bacterial
XX infection by a 7-339 peptide or relative bacteria, comprises a
XX 7-339 peptide and peptide membrane-associating element.
XX
PS Claim 7; Page 57; 64pp; English.

CC The present invention describes an antibacterial compound (I), comprising
CC a mixture of glycopeptide and peptide membrane-associating elements
CC (i) comprises the formula V LW X, where V is a glycopeptide moiety that
CC binds to peptidoglycan synthesis in bacteria, L is a linking group,
CC W is a peptidic membrane associating element, and X is H or a membrane
CC insertion element. Also described is (ii) a method of treating or preventing
CC a bacterial infection, comprising the administration of (I), and (3) use
CC of (I) in the manufacture of a medicament for the treatment or prevention
CC of a bacterial infection. (ii) are used in the manufacture of a medicament
CC for the treatment or prophylaxis of a bacterial infection in a human or
CC animal body, including both the oral, intravenous and intraperitoneal
CC treatment. Exemplary bacteria include: *Escherichia coli*, *Staphylococcus*
CC *epidermidis* sp., *Staphylococcus aureus* sp., *Streptococcus* sp., *Streptococcus*
CC *pyogenes* sp., *Streptococcus pneumoniae* sp., *Pseudomonas* sp., *Actinomyces* sp.,
CC *Haemophilus* sp., *Clostridium* sp., *Salmonella* sp., particularly antibiotic resistant
CC bacterial strains. (ii) are also useful as wound treatment agents to
CC prevent adhesion of bacteria to matrix proteins, especially fibrinogen,
CC exposed in wound tissue; and for prophylactic use in dental treatment as
CC an alternative to, or in conjunction with, antibiotic prophylaxis. (i)
CC has a higher binding to bacterial membranes which have a higher
CC proportion of acidic phospholipids than the eukaryotic organisms, also
CC having a higher proportion of membrane associated biosynthesis proteins.
CC Vancomycin shows an enhanced antibacterial activity upon derivatization
CC with (i) and is effective to treat the antibiotic resistant bacterial
CC strains. ABB81240 to ABB81244 represent peptides given in the
CC exemplification of the present invention.

XX
SQ Sequence 16 AA;
Query Match 92.9%; Score 77; E: 23; Length 16;

Best Local Similarity 49.0%; Prod No. 14;
Matches 10, Conservation 1, Mismatches 1, Gaps 1

CY 1 DGPFFRFFRFFSSSS 15
||||| ||||| |||||
DB 1 DGPFFRFFRFFSSSS 15

RESULT 7
AAW45882
ID AAW45882 standard; peptide; 14 AA.
XX
AC AAW45882;
XX
CT 30-JUN-1998 (first entry)
XX
DE Peptide membrane binding element.
XX
KW Membrane binding element; thrombotic disease; inflammation;
XX Complement-related disease; soluble peptide.
XX
OS Synthetic.
XX
PN WO9902454 A2.
XX
PD 22-JAN-1998.
XX
PE 08-JUL-1997; 97WO-EP03715.
XX
PF 15-JUL-1996; 96GR-0014971.
XX
PG (ACPR-) APPROTECH PLC.
XX
PI Delf I, Messakowska DEL, Smith PAG;
XX
PP WPI, 1999 110524/10.
XX
PT Derivative of soluble poly-peptides, bonded to low affinity
XX membrane binding groups - useful for treating complement-related and
XX thrombotic diseases, providing improved localisation at cellular
XX membranes
XX
PS Claim 11; Page 70; 75pp; English.

CC The present peptide sequence represents a specifically claimed membrane
CC binding element. The invention relates to a soluble derivative (A) of a
CC soluble glycopeptide (B), which comprises at least a heterologous
CC membrane-binding element (W) of low membrane affinity, covalently
CC associated with (i) MHC interact, independently and with thermodynamic
CC activity, with components of cellular artificial membrane exposed
CC to extracellular fluids (A) are used to treat disorders treatable with
CC (ii) itself, specifically inflammation or any other complement-related
CC disorder in a neurological disease, graft rejection, myocardial
CC infarction, stroke, the related arthritis and many others, including
CC application in swelling diseases and thrombotic diseases but also to
CC treat allergy, inflammatory diseases, to treat leukaemia or asthma and as
CC immuno-moieties for treating multiple sclerosis. (A) are administered
CC orally, typically, by injection and inhalation at a dose of preferably
CC 0.1 to 100 mg/kg/day.

XX
SQ Sequence 14 AA;
Query Match 49.0%; Score 40; E: 19; Length 14;
Best Local Similarity 70.0%; Prod No. 14;
Matches 10, Conservation 1, Mismatches 1, Gaps 1

CY 1 DGPFFRFFRFFSSSS 15
||||| ||||| |||||
DB 1 DGPFFRFFRFFSSSS 15

RESULT 8
ABB81241

colitis from presence of perinuclear
antibodies reacting with histone H1 -
method using H1 or its fragments
English.
P01AA023490 99 word fragment from the N-terminal
sequence H1S-1. The invention relates to diagnosis
and comprises treating a patient's sample with
perinuclear anti-histone H1 cytoplasmic
fragments and detecting formation of a complex
between the sample and the fragments. The invention
relates to human H1. The same method can also be
applied to ulcerative colitis. The invention
comprises a PANCA positive ulcerative
colitis diagnosis of H1 or its fragments.
Treatment of serum with H1 or its PANCA-
binding complex formed and returning the
serum to its composition comprising H1, or its
fragments, or a combination thereof, for prevention of ulcerative
colitis or H1 or tolerances, including fragments
of H1, including peptides diagnosed as being
specifically used. Diagnose the PANCA
and ulcerative colitis. The invention is based
on H1A present in most ulcerative colitis
patients H1.

AA: Score 40; EP 12; Length 15;
AA: Pred. No. 18;
Mismatches 0; Gaps 0;
Caps 0;
40: 15 AA.
7
P1P2
AA: H1-like antigen, human; human;
ulcerative colitis; H1S-1; PANCA; diagnosis;
H1 cytoplasmic anti-H1A form.

40: 15 AA.
40: 15 AA.

H1 bacteroides antigen as targets for the

diagnosis, prevention and treatment of ulcerative colitis
Example 3; Page 67, 134pp; English.
The invention provides a method for the diagnosis, prevention and
treatment of ulcerative colitis (UC) using histone H1-like antigen, a
porin antigen or a bacteroides antigen as a target antigen. The novel
method of diagnosing UC in a subject suspected of having inflammatory
bowel disease (IBD) comprises: (a) obtaining a sample from the subject;
(b) contacting the sample with a histone H1-like antigen, or perinuclear
anti-neutrophil cytoplasmic antibody (PANCA) reactive fragment, to form
a complex of the histone H1-like antigen, or the PANCA reactive
fragment, and antibody to the histone H1-like antigen; and (c) detecting
the presence or absence of the complex. Alternatively, if the
complex indicates that the subject has UC, the PANCA reactive histone
H1-like antigen, porin antigen and bacteroides antigen are useful in the
diagnosis, prevention and treatment of UC. The methods can also be used
for identifying agents useful for treating UC. Sequences AA14541-1, 1
represent peptides spanning the human histone H1S-1 gene product. These
were assayed for H1AUC-1 and H1AUC-2 binding to identify PANCA reactive
peptides.
SQ Sequence 15 AA;
Query Match 48.4%; Score 40; EP 12; Length 15;
Percent Similarity 58.3%; Field No. 18;
Matches 7; Conservative 2; Mismatched 3; Indels 0; Gaps 0

QV ? PPKKKKSPKPS 14
||| ||| |||
Db 3 PPKSAKVTPEKA 14

RESULT 14
AAV57345
ID AAV57345 standard; peptide; 15 AA.
XX AC AAV57345;
XX DT 13-JUN-2000 (first entry
XX DE Human histone H1 PANCA-reactive peptide.
XX KW Ulcerative colitis; inflammatory bowel disease; porin antigen;
XX KW PANCA; perinuclear anti-neutrophil cytoplasmic antibody; H1AUC-1;
XX KW Histone H1; isoform; H1AUC-2.
XX OS Homo sapiens.
XX PN US6033864-A.
XX PP 07-MAR-2000.
XX FF 12-MAR-1998; 9805 0041889.
XX PR 12-APR-1994; 9405 0057846.
XX PR 11-APR-1997; 9703 0837058.
XX PA (REGC) UNIV CALIFORNIA.
XX PI Chavay O, Braun J;
XX XX WPI; 2000.255695/22.
XX XX

Diagnosing ulcerative colitis or susceptibility by detecting perinuclear
formation between microbial porin antigen and perinuclear
anti-neutrophil cytoplasmic autoantibodies -
Example 3; Column 30; 49pp; English.
The invention provides a method for diagnosing ulcerative colitis in a
subject suspected of having inflammatory bowel disease. The method
comprises reacting a patient sample with a porin antigen, H1AUC-1 or

CC immunologically reactive with pMCA (antibody anti-peptide)
 CC cytoplasmic antibodies) and defining formation of a Ag pMCA complex
 CC as indicative of ulcerative colitis. The method is used to diagnose
 CC ulcerative colitis or susceptibility to it. Sequences AAY57341-351
 CC represent pMCA-reactive peptides, derived from human histone H1
 XX
 SQ Sequence 15 AA;

QY 3 PPKKKKKSPSKS 14
 DB 3 PPKKKKKSPSKS 14

RESULT 15
 AAB26821
 ID AAB26821 standard; peptide: 9 AA.

XX
 AC AAB26821;
 XX
 DT 23 JAN 2001 (first entry)
 XX
 DE Peptidic membrane binding element.

XX Organ perfusion; transplantation, storage, antiinflammatory;
 KW immunosuppressive; vasotropic; complement activation inhibitor;
 KW allograft rejection; ischaemia reperfusion injury.
 XX
 OS Synthetic.

XX W0206053007-A1.
 XX 14-SEP-2000.
 XX 08-MAR-2000; 2000WO GB00834.
 XX 10-MAR-1999; 99GR-0006503.
 XX (ADPR-) ADPROTECH LTD.

XX Smith RAG, Pratt JP, Sacks SH;
 XX WPI; 2000-01-20/57.

XX Preparation for perfusing organ prior to transplantation or storage
 PT comprises soluble binding of a cell the polypeptide which comprises
 PT two heterologous membrane binding elements with low membrane affinity

PS Example 2; Page 20; 47pp; English.

XX The present invention relates to formulations and preparations for
 CC perfusing an organ prior to transplantation or storage. The preparation
 CC comprises a soluble derivative of a polypeptide, which has two or more
 CC heterologous membrane binding elements. The membrane binding elements are
 CC capable of interacting, independently and with thermodynamic additivity,
 CC with membrane components of the organ exposed to extra-cellular perfusion
 CC fluids, and a flush storage solution. The preparation exhibits
 CC antiinflammatory, immunosuppressive and vasotropic activity and works as
 CC a complement activation inhibitor and an inhibitor of cytotoxic T
 CC lymphocyte activity. The preparation is used for preparing an organ prior
 CC to transplantation, storage and for prevention, treatment or
 CC amelioration of a disease or disorder associated with inflammation,
 CC inappropriate complement activation or inappropriate activation of
 CC coagulant or thrombotic processes prior to, during or after
 CC transplantation or storage of an organ. The preparation is useful for
 CC treating ischaemic and acute allograft rejection of transplanted organs
 CC such as kidney, heart, liver or lungs, ischaemia reperfusion injury in
 CC transplanted organs, xenograft rejection and corneal graft rejection. The
 CC present sequence represents a peptidic membrane binding element used in

CC An example of the preparation of the invention:
 XX Sequence 9 AA;

Query March 47.0%; Score 39; DB 21; Length 9;
 Best Local Similarity 77.9%; Pred. NO. 7.9e+05;
 Matches 7; Conservative 0; Mismatches 2; Indels 0;

QY 3 PPKKKKKSP 11
 DB 3 PPKKKKKSP 11

Search completed: March 3, 2003, 06:44:31
 Job time : 48 secs


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1 MOLECULE TYPE: peptide
2 FEATURE:
3 NAME/KEY: Modified site
4 LOCATION: 13
5 OTHER INFORMATION: /SUBJECT: "OTHER"
6 OTHER INFORMATION: /SUBJECT: "Xaa = Ile, Met, Thr, Asn, Lys,
7 OTHER INFORMATION: Ser or Arg"
8 FEATURE:
9 NAME/KEY: Modified site
10 LOCATION: 14
11 OTHER INFORMATION: /PRODUCT: "OTHER"
12 OTHER INFORMATION: /NOTE: "Xaa = Cys, Ala, Ser or Gly"
13 US-08 910-386A-53
14
15 Query Match 40.4%, Score 43, DB 9, Length 14;
16 Best Local Similarity 72.0%, Pred. No. 18;
17 Matches 9, Conservative 1, Mismatches 1, Indels 1, Gaps 0;
18
19 QY 3 KKKKKKSPSK 13
20 I|||||
21 DB 2 KKKKKKSPSK 11
22 I|||||
23
24 RESULT 2
25 US-09-967-772-16
26 Sequence 16, Application US/09067072
27 Patent No. US063004549A1
28 GENERAL INFORMATION:
29 APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
30 APPLICANT: TS'EN, Roger
31 APPLICANT: GONZALES, Jesus
32 TITLE OF INVENTION: ISOLATION OF TRANSMEMBRANE PROTEINS BY USING NETHIN-1
33 FILE REFERENCE: US063004549A1
34 CURRENT APPLICATION NUMBER: US/09067072
35 PRIOR FILING DATE: 2001-09-28
36 PRIOR FILING DATE: 1999-12-13
37 PRIOR APPLICATION NUMBER: US 08/063,483
38 PRIOR FILING DATE: 1994-10-10
39 PRIOR APPLICATION NUMBER: PCT/US96/10060
40 PRIOR FILING DATE: 1996-03-05
41 FILE APPLICATION NUMBER: US 08/411,377
42 PRIOR FILING DATE: 1998-06-07
43 NUMBER OF SEQ ID NOS: 22
44 SOFTWARE: PatentIn version 3.0
45 SEQ ID NO: 16
46 LENGTH: 15
47 TYPE: PPT
48 ORGANISM: Artificial sequence
49 FEATURE:
50 OTHER INFORMATION: Isolation modification sequence
51 US-09 967-772-16
52
53 Query Match 47.0%, Score 50, DB 9, Length 15;
54 Best Local Similarity 80.0%, Pred. No. 18;
55 Matches 9, Conservative 1, Mismatches 1, Indels 1, Gaps 0;
56
57 QY 4 KKKKKKSPSK 13
58 I|||||
59 DB 2 KKKKKKSPSK 11
60 I|||||
61
62 RESULT 3
63 US-09-945-249-84
64 Sequence 84, Application US/09045249
65 Patent No. US063004549A1
66 GENERAL INFORMATION:
67 APPLICANT: BERLIN, VIVIAN
68 APPLICANT: LAVAGNINI, VERONIQUE
69 APPLICANT: SMITH, SUSAN E.
70 TITLE OF INVENTION: ANALOG AND ANALOGS FOR IDENTIFYING AND TREATING
71 TITLE OF INVENTION: ANALOGS AND ANALOGS FOR IDENTIFYING AND TREATING
72 FILE REFERENCE: MIV-074,06

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1 CURRENT APPLICATION NUMBER: US/09045249
2 CURRENT FILING DATE: 2001-08-31
3 PRIOR APPLICATION NUMBER: US 08/411,390
4 PRIOR FILING DATE: 2001-01-13
5 PRIOR APPLICATION NUMBER: US/771,212
6 PRIOR FILING DATE: 1997-12-20
7 PRIOR APPLICATION NUMBER: US/081,310
8 PRIOR FILING DATE: 1996-04-11
9 NUMBER OF SEQ ID NOS: 80
10 SOFTWARE: PatentIn Ver. 2.1
11 SEQ ID NO: 94
12 LENGTH: 15
13 TYPE: PPT
14 ORGANISM: Artificial Sequence
15 FEATURE:
16 OTHER INFORMATION: Description of Artificial Sequence: Peptide that
17 OTHER INFORMATION: referred to as "Xaa" in the context of this database
18 OTHER INFORMATION: substrates
19 US-09-945-249-84
20
21 Query Match 47.0%, Score 50, DB 9, Length 15;
22 Best Local Similarity 80.0%, Pred. No. 18;
23 Matches 9, Conservative 1, Mismatches 1, Indels 1, Gaps 0;
24
25 QY 4 KKKKKKSPSK 13
26 I|||||
27 DB 2 KKKKKKSPSK 11
28 I|||||
29
30 RESULT 4
31 US-09-784-818-2
32 Sequence 2, Application US/09094818
33 Patent No. US063004549A1
34 GENERAL INFORMATION:
35 APPLICANT: Verckin Co., Inc.
36 APPLICANT: GINSBERG, Christopher M.
37 APPLICANT: BERGMAN, Jeffrey M.
38 TITLE OF INVENTION: PEPTIDE-PROTEIN TRANSDOMAIN INHIBITORS
39 FILE REFERENCE: US063004549A1
40 CURRENT APPLICATION NUMBER: US/09094818
41 PRIOR FILING DATE: 2001-02-16
42 FILE APPLICATION NUMBER: US/09094818
43 PRIOR FILING DATE: 2000-02-18
44 NUMBER OF SEQ ID NOS: 21
45 SOFTWARE: PatentIn Version 4.0
46 SEQ ID NO: 2
47 LENGTH: 15
48 TYPE: PPT
49 ORGANISM: Artificial Sequence
50 FEATURE:
51 OTHER INFORMATION: Completely synthetic sequence
52 US-09-784-818-2
53
54 Query Match 47.0%, Score 50, DB 9, Length 15;
55 Best Local Similarity 80.0%, Pred. No. 18;
56 Matches 9, Conservative 1, Mismatches 1, Indels 1, Gaps 0;
57
58 QY 4 KKKKKKSPSK 13
59 I|||||
60 DB 2 KKKKKKSPSK 11
61 I|||||
62
63 RESULT 5
64 US-09-770-967-2
65 Sequence 84, Application US/090770967
66 Patent No. US063004549A1
67 GENERAL INFORMATION:
68 APPLICANT: Merck & Co., Inc.
69 APPLICANT: PINSKY, Christopher J.
70 APPLICANT: BERGMAN, Jeffrey M.
71 TITLE OF INVENTION: Inhibitors of protein synthesis
72 TITLE OF INVENTION: Inhibitors of protein synthesis
73 FILE REFERENCE: 0406
74 CURRENT APPLICATION NUMBER: US/090770,967

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; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homosapien
US-09-819-522-2

Query Match      47.0% Score 19; DP 19; Length 15
Best Local Similarity 80.0% Pred. No. 18;
Matches 8; Conservative 1; Mismatches 1; Gaps 0;

QY 4 KKKKKKPSK 13
DE 2 KKKKKSVK 11

RESULT 8
US-09-757-251-3
; Sequence 3, Application US/095725;
; Patent No. US600804217A1
; GENERAL INFORMATION:
; APPLICANT: Merck & Co., Inc.
; APPLICANT: S. Jane deSolms
; APPLICANT: Suzanne C. MacTough
; APPLICANT: Anthony W. Shaw
; TITLE OF INVENTION: INHIBITORS OF PHENYL-PROTEIN TRANSFERASE
; FILE REFERENCE: 20604Y
; CURRENT APPLICATION NUMBER: US/09/757,251;
; PRIOR FILING DATE: 2001-01-09
; PRIOR APPLICATION NUMBER: 60/175,784
; PRIOR FILING DATE: 2000-01-12
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Completely Synthetic Amino Acid
US-09-757-251-3

Query Match      47.0% Score 19; DP 19; Length 15;
Best Local Similarity 80.0% Pred. No. 18;
Matches 8; Conservative 1; Mismatches 1; Gaps 0;

QY 4 KKKKKKPSK 13
DE 2 KKKKKSVK 11

RESULT 9
US-09-784-897A-2
; Sequence 2, Application US/09784897A
; Patent No. US2002052363A1
; GENERAL INFORMATION:
; APPLICANT: Merck & Co., Inc.
; APPLICANT: Dinsmore, Christopher J.
; APPLICANT: Bergman, Jeffrey M.
; TITLE OF INVENTION: PHENYL-PROTEIN TRANSFERASE INHIBITORS
; FILE REFERENCE: 20497
; CURRENT APPLICATION NUMBER: US/09/784,897A
; CURRENT FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: 60/183,449
; PRIOR FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Completely Synthetic sequence
US-09-784-897A-2
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; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homosapien
US-09-819-522-2

Query Match      47.0% Score 19; DP 19; Length 15;
Best Local Similarity 80.0% Pred. No. 18;
Matches 8; Conservative 1; Mismatches 1; Gaps 0;

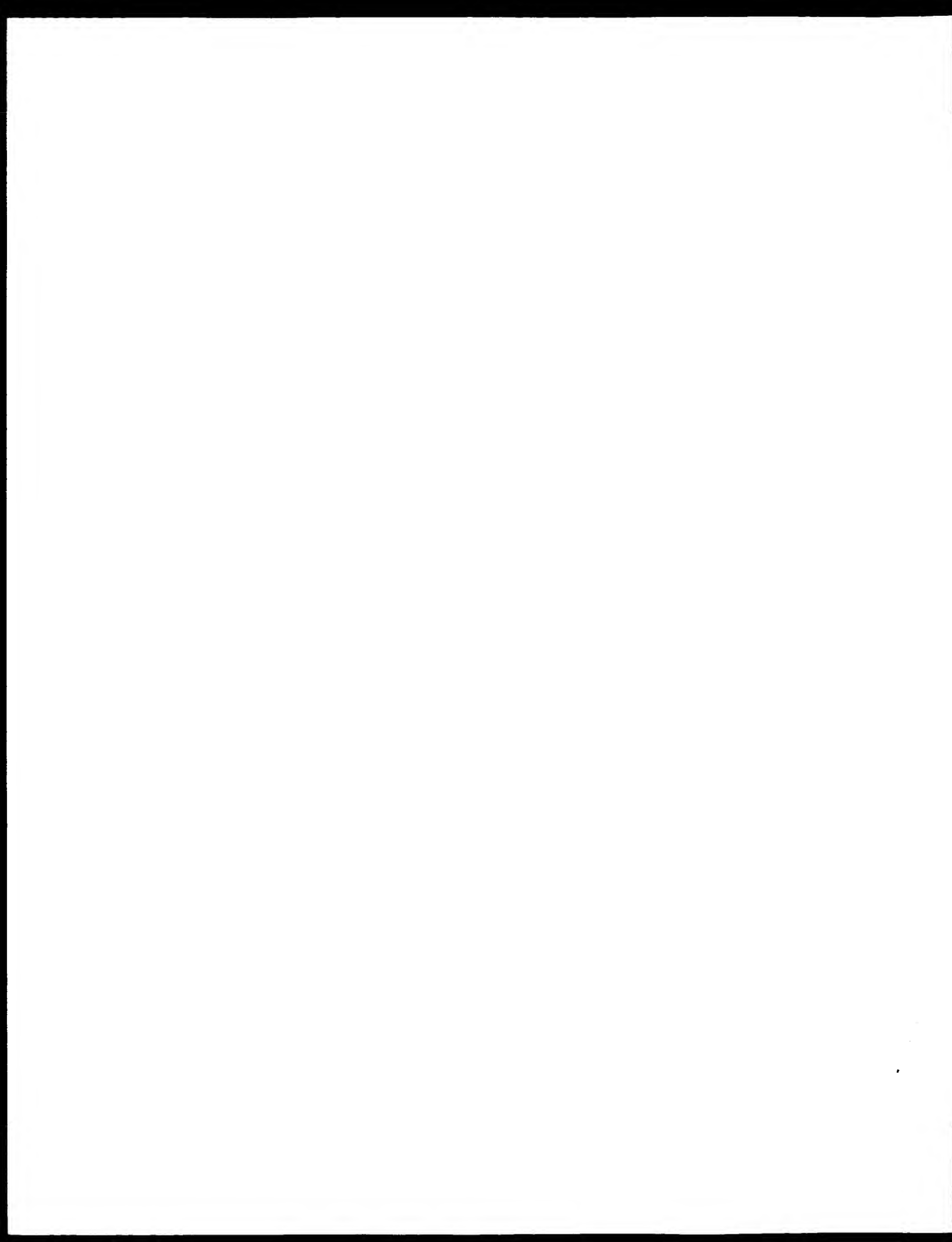
QY 4 KKKKKKPSK 13
DE 2 KKKKKSVK 11

RESULT 8
US-09-757-251-3
; Sequence 3, Application US/095725;
; Patent No. US600804217A1
; GENERAL INFORMATION:
; APPLICANT: Merck & Co., Inc.
; APPLICANT: S. Jane deSolms
; APPLICANT: Suzanne C. MacTough
; APPLICANT: Anthony W. Shaw
; TITLE OF INVENTION: INHIBITORS OF PHENYL-PROTEIN TRANSFERASE
; FILE REFERENCE: 20604Y
; CURRENT APPLICATION NUMBER: US/09/757,251;
; PRIOR FILING DATE: 2001-01-09
; PRIOR APPLICATION NUMBER: 60/175,784
; PRIOR FILING DATE: 2000-01-12
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Completely Synthetic Amino Acid
US-09-757-251-3

Query Match      47.0% Score 19; DP 19; Length 15;
Best Local Similarity 80.0% Pred. No. 18;
Matches 8; Conservative 1; Mismatches 1; Gaps 0;

QY 4 KKKKKKPSK 13
DE 2 KKKKKSVK 11

RESULT 9
US-09-784-897A-2
; Sequence 2, Application US/09784897A
; Patent No. US2002052363A1
; GENERAL INFORMATION:
; APPLICANT: Merck & Co., Inc.
; APPLICANT: Dinsmore, Christopher J.
; APPLICANT: Bergman, Jeffrey M.
; TITLE OF INVENTION: PHENYL-PROTEIN TRANSFERASE INHIBITORS
; FILE REFERENCE: 20497
; CURRENT APPLICATION NUMBER: US/09/784,897A
; CURRENT FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: 60/183,449
; PRIOR FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Completely Synthetic sequence
US-09-784-897A-2
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Db 3 PKRSAXTPKKA 14
RESULT 2
US 08-913-068-19
Sequence 19, Application NO/98413064
Patent No. 5967743
GENERAL INFORMATION:
APPLICANT: Braun, Jonathan P.
APPLICANT: Targan, Stephan P.
APPLICANT: Eysa, Mark
TITLE OF INVENTION: Diabetes, Prevention and Treatment of
TITLE OF INVENTION: Microarray Analysis, and Clinical Subtypes Thereof, Using
TITLE OF INVENTION: Histone H1
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 100
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
SOFTWARE: Patent in Release #10, Version #1.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/98/413,064
FILING DATE: 27 APR 1995
CLASSIFICATION: 435
PRIORITY INFORMATION:
PRIORITY NUMBER: 08/07,622,011
FILING DATE: 16-FEB-1993
CLASSIFICATION: 435
APPLICATION NUMBER: US 07/622,011
FILING DATE: ABANDONED
CLASSIFICATION: 435
APPLICATION NUMBER: PCT/US/91/02650
FILING DATE: 18-APR-1991
CLASSIFICATION: 435
APPLICATION NUMBER: 435
FILING DATE: 20-NOV-1990
CLASSIFICATION: 435
APPLICATION NUMBER: US 07/615,715
FILING DATE: 20-NOV-1990
CLASSIFICATION: 435
APPLICATION NUMBER: US 07/510,706
FILING DATE: 19-APR-1992 (ABANDONED)
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: PARKER, DAVID L.
REGISTRATION NUMBER: 32,165
REFERENCE/AGENT NUMBER: ITSD:432/PAR
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 793-2479
TELEX: 79-0924
INFORMATION FOR SEQ ID NO: 77:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Peptide
US 08 429-964-77
Query Match 48.2% Score 40; DB 3; Length 15;
Best Local Similarity 55.3%, Freq. No. 1,
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
Db 3 PKRSAXTPKKA 14
RESULT 3
US 08 429 964 77
Sequence 77, Application NO/98413064
Patent No. 5967743
GENERAL INFORMATION:
APPLICANT: BROWN, MICHAEL S.
APPLICANT: GOLSTEIN, JOSEPH L.
APPLICANT: REISS, YUVAL
APPLICANT: JAMES, GUY L.
TITLE OF INVENTION: METHODS FOR THE IDENTIFICATION OF FARNESYL
TITLE OF INVENTION: TRANSFEASE INHIBITORS
NUMBER OF SEQUENCES: 85
CORRESPONDENCE ADDRESS:
ADDRESSEE: ARNOLD, WHITE & NUPPKE
STREET: P.O. BOX 4433
CITY: HOUSTON
STATE: TEXAS
COUNTRY: UNITED STATES OF AMERICA
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

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US-08-985-124A-1
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/032,438
FILING DATE: 05-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Muthard, David A
REGISTRATION NUMBER: 35,297
REFERENCE/DOCKET NUMBER: 19833Y
TELECOMMUNICATION INFORMATION:
TELEPHONE: 908-594-3903
TELEFAX: 908-594-4720
TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-985-337A-1
Query Match: 47.5% Score 39; DP 2; Length 15
Best Local Similarity 90.0%; Pred. No. 7;
Matches 9; Conservative 1; Mismatches 1; Indels 0
CY 4 KKKYKPSKY 13
DB 2 KKKYKPSKY 11
RESULT 6
US-08-985-124A-1
Sequence 1, Application US/6895124A
Patent No. 5972966
GENERAL INFORMATION:
APPLICANT: desolms, S. Jace
TITLE OF INVENTION: INHIBITORS OF FARNESYL-PROTEIN
TRANSFERASE
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merck & Co., Inc.
STREET: P.O. Box 2000, 126 E. Lincoln Ave.
CITY: Rahway
STATE: NJ
COUNTRY: USA
ZIP: 07065-0900
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/68/985,124A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/032,438
FILING DATE: 05-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Muthard, David A
REGISTRATION NUMBER: 35,297
REFERENCE/DOCKET NUMBER: 19833Y
TELECOMMUNICATION INFORMATION:
TELEPHONE: 908-594-3903
TELEFAX: 908-594-4720
TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein

US-08-985-124A-1
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/032,438
FILING DATE: 05-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Muthard, David A
REGISTRATION NUMBER: 35,297
REFERENCE/DOCKET NUMBER: 19833Y
TELECOMMUNICATION INFORMATION:
TELEPHONE: 908-594-3903
TELEFAX: 908-594-4720
TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-985-337A-1
Query Match: 47.5% Score 39; DP 2; Length 15
Best Local Similarity 90.0%; Pred. No. 7;
Matches 9; Conservative 1; Mismatches 1; Indels 0
CY 4 KKKYKPSKY 13
DB 2 KKKYKPSKY 11
RESULT 6
US-08-985-124A-1
Sequence 1, Application US/6895124A
Patent No. 5972966
GENERAL INFORMATION:
APPLICANT: desolms, S. Jace
TITLE OF INVENTION: INHIBITORS OF FARNESYL-PROTEIN
TRANSFERASE
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merck & Co., Inc.
STREET: P.O. Box 2000, 126 E. Lincoln Ave.
CITY: Rahway
STATE: NJ
COUNTRY: USA
ZIP: 07065-0900
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/68/985,124A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/032,438
FILING DATE: 05-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Muthard, David A
REGISTRATION NUMBER: 35,297
REFERENCE/DOCKET NUMBER: 19833Y
TELECOMMUNICATION INFORMATION:
TELEPHONE: 908-594-3903
TELEFAX: 908-594-4720
TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein

US 09-214-913-37

Query Match: 47.03, Score 327, EB 2, Length 15,
Best Local Similarity: 80.03, Field No. 7,
Matches: 8, Conservative: 1, Mismatches: 1, Indels: 0, Gaps: 0

QY 4 PPTPTPTPTPT 13
DB 2 PPTPTPTPT 11

RESULT 7

US 09-985-320A-1
Sequence 1, Application US/09095320A
Patent No. 5977114
GENERAL INFORMATION:
APPLICANT: Ciccarone, Terrence M.
APPLICANT: Halczenko, Wasy
APPLICANT: Halczenko, John H.
APPLICANT: Luma, Jr., William C.
APPLICANT: Storker, Gerald E.
APPLICANT: Stump, Craig A.
APPLICANT: Williams, Theresa M.
TITLE OF INVENTION: INHIBITORS OF PARMEYLY PROTEIN
TITLE OF INVENTION: TRANSFERASE
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Mark & Co., Inc.
STREET: P.O. Box 2000, 126 E. Lincoln Ave.
CITY: Rahway
STATE: NJ
COUNTRY: USA
ZIP: 07065-0900

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/98/320A
FILING DATE: 05/DEC/1996
CLASSIFICATION: 514
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 60/032,579
FILING DATE: 06 DEC 1996
ATTORNEY/AGENT INFORMATION:
NAME: Markard, David A.
REGISTRATION NUMBER: 35,297
REFERENCE/DOCKET NUMBER: 100409
TELECOMMUNICATION INFORMATION:
TELEPHONE: 908-594-3963
TELEFAX: 908-594-4720
TELEX:

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-985-320A-1
Query Match: 47.03, Score 327, EB 2, Length 15,
Best Local Similarity: 80.03, Field No. 7,
Matches: 8, Conservative: 1, Mismatches: 1, Indels: 0, Gaps: 0

QY 4 PPTPTPTPTPT 13
DB 2 PPTPTPTPT 11

RESULT 8

US-09-984-732A-1

US 09-214-913-37

Sequence 1, Application US/09095320A
Patent No. 6015817
GENERAL INFORMATION:
APPLICANT: Halczenko, Wasy
APPLICANT: Stump, Craig A.
TITLE OF INVENTION: INHIBITORS OF PARMEYLY PROTEIN
TITLE OF INVENTION: TRANSFERASE
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Mark & Co., Inc.
STREET: P.O. Box 2000, 126 E. Lincoln Ave.
CITY: Rahway
STATE: NJ
COUNTRY: USA
ZIP: 07065-0900

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/98/984,732A
FILING DATE: 05/DEC/1996
CLASSIFICATION: 514
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 60/032,106
FILING DATE: 05/DEC/1996
ATTORNEY/AGENT INFORMATION:
NAME: Markard, David A.
REGISTRATION NUMBER: 35,297
REFERENCE/DOCKET NUMBER: 100409
TELECOMMUNICATION INFORMATION:
TELEPHONE: 908-594-3963
TELEFAX: 908-594-4720
TELEX:

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-984-732A-1
Query Match: 47.03, Score 327, EB 2, Length 15,
Best Local Similarity: 80.03, Field No. 7,
Matches: 8, Conservative: 1, Mismatches: 1, Indels: 0, Gaps: 0

QY 4 PPTPTPTPTPT 13
DB 2 PPTPTPTPT 11

RESULT 9

US-09-195-578-13
Sequence 13, Application US/09195578
Patent No. 6054466
GENERAL INFORMATION:
APPLICANT: Ciccarone, Terrence M.
APPLICANT: Ciccarone, Terrence M.
APPLICANT: Ciccarone, Terrence M.
APPLICANT: Ciccarone, Terrence M.
TITLE OF INVENTION: INHIBITORS OF PARMEYLY PROTEIN
TITLE OF INVENTION: TRANSFERASE
FILE REFERENCE: 000000
CURRENT APPLICATION NUMBER: 09/019,578
CURRENT FILING DATE: 1998-11-18
EARLIER APPLICATION NUMBER: 09/019,578
EARLIER FILING DATE: 1997-12-04
NMPFF: 09/019,578
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 13
LENGTH: 15
TYPE: PRT

Mon Mar 3 10:55:18 2003

Search completed March 3, 2003, 06:47:20
 Job time : 17.6667 secs

QY 4 KKKKKSPSK 13
 DB 2 KKKKKSKTK 11

RESULT 14

US-09-456-153-2
 : Sequence 2, Application US/09456153
 : Patent No. 6284755
 : GENERAL INFORMATION:
 : APPLICANT: Desolms, S. Jane
 : APPLICANT: Graham, Samuel L.
 : APPLICANT: Shaw, Anthony W.
 : APPLICANT: Ciccarone, Terrence M.
 : APPLICANT: Storker, Gerald E.
 : TITLE OF INVENTION: INHIBITORS OF TRENIL PROTEIN
 : TITLE OF INVENTION: TRANSFERASE
 : FILE REFERENCE: 20312Y
 : CURRENT APPLICATION NUMBER: US/09/456,153
 : CURRENT FILING DATE: 1999-12-07
 : EARLIER APPLICATION NUMBER: US 60/111,416
 : EARLIER FILING DATE: 1998-12-08
 : EARLIER APPLICATION NUMBER: US 60/129,292
 : EARLIER FILING DATE: 1999-04-14
 : NUMBER OF SEQ ID NOS: 21
 : SOFTWARE: FastSeq for Windows Version 3.0
 : SEQ ID NO 2
 : LENGTH: 15
 : TYPE: PRT
 : ORGANISM: Homosapien
 US-09-456-153-2

Query Match 47.0%; Score 39; DB 4; Length 15;
 Best Local Similarity 80.0%; Pred. No. 7;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 KKKKKSPSK 13
 DB 2 KKKKKSKTK 11

RESULT 15

US-09-167-180-13
 : Sequence 13, Application us/09167180
 : Patent No. 6297239
 : GENERAL INFORMATION:
 : APPLICANT: desolms, S. Jane
 : APPLICANT: Hutchinson, John H.
 : APPLICANT: Shaw, Anthony W.
 : APPLICANT: Graham, Samuel L.
 : APPLICANT: Ciccarone, Terrence M.
 : APPLICANT: Merck & Co., Inc.
 : TITLE OF INVENTION: INHIBITORS OF TRENIL PROTEIN TRANSFERASE
 : FILE REFERENCE: 19928Y
 : CURRENT APPLICATION NUMBER: US/09/167,180
 : CURRENT FILING DATE: 1998-10-06
 : EARLIER APPLICATION NUMBER: 60/662,660
 : EARLIER FILING DATE: 1997-10-08
 : NUMBER OF SEQ ID NOS: 26
 : SOFTWARE: FastSeq for Windows Version 3.0
 : SEQ ID NO 13
 : LENGTH: 15
 : TYPE: PRT
 : ORGANISM: Homosapien
 US-09-167-180-13

Query Match 47.0%; Score 39; DB 4; Length 15;
 Best Local Similarity 80.0%; Pred. No. 7;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 KKKKKSPSK 13
 DB 2 KKKKKSKTK 11

bioactive version 1.0.0
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us-09-214-913-38

1. 1997-1998 / Search and 1997-1998
with 1997-1998
1997-1998 / 1997-1998

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1997-1998

1. 1997-1998 / Search and 1997-1998
with 1997-1998
1997-1998 / 1997-1998

SUMMARIES

IP	IP	Description
1	A12971	heparin-binding lectin - human (fragment)
2	A27803	myosin light chain - turkey (fragment)
3	A27803	myosin light chain - turkey (fragment)
4	A27803	myosin light chain - turkey (fragment)
5	A27803	myosin light chain - turkey (fragment)
6	A27803	myosin light chain - turkey (fragment)
7	A27803	myosin light chain - turkey (fragment)
8	A27803	myosin light chain - turkey (fragment)
9	A27803	myosin light chain - turkey (fragment)
10	A27803	myosin light chain - turkey (fragment)
11	A27803	myosin light chain - turkey (fragment)
12	A27803	myosin light chain - turkey (fragment)
13	A27803	myosin light chain - turkey (fragment)
14	A27803	myosin light chain - turkey (fragment)
15	A27803	myosin light chain - turkey (fragment)
16	A27803	myosin light chain - turkey (fragment)
17	A27803	myosin light chain - turkey (fragment)
18	A27803	myosin light chain - turkey (fragment)
19	A27803	myosin light chain - turkey (fragment)
20	A27803	myosin light chain - turkey (fragment)
21	A27803	myosin light chain - turkey (fragment)
22	A27803	myosin light chain - turkey (fragment)
23	A27803	myosin light chain - turkey (fragment)
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28	A27803	myosin light chain - turkey (fragment)
29	A27803	myosin light chain - turkey (fragment)
30	A27803	myosin light chain - turkey (fragment)
31	A27803	myosin light chain - turkey (fragment)
32	A27803	myosin light chain - turkey (fragment)
33	A27803	myosin light chain - turkey (fragment)
34	A27803	myosin light chain - turkey (fragment)
35	A27803	myosin light chain - turkey (fragment)
36	A27803	myosin light chain - turkey (fragment)
37	A27803	myosin light chain - turkey (fragment)
38	A27803	myosin light chain - turkey (fragment)
39	A27803	myosin light chain - turkey (fragment)
40	A27803	myosin light chain - turkey (fragment)
41	A27803	myosin light chain - turkey (fragment)
42	A27803	myosin light chain - turkey (fragment)
43	A27803	myosin light chain - turkey (fragment)
44	A27803	myosin light chain - turkey (fragment)
45	A27803	myosin light chain - turkey (fragment)

30	19	22.9	13	2	A46443
31	19	22.9	14	2	CHC108
32	19	22.9	14	2	I39253
33	19	22.9	14	2	H64008
34	19	22.9	14	2	PAC036
35	19	22.9	15	2	H56078
36	19	22.9	15	2	S67118
37	19	22.9	15	2	G49255
38	19	22.9	15	2	FX0031
39	19	22.9	15	2	H51541
40	18	21.7	6	2	PT0280
41	18	21.7	9	2	PC7074
42	18	21.7	10	1	PHLM38
43	18	21.7	10	2	A49147
44	18	21.7	11	2	G61437
45	18	21.7	11	2	PH0919

ALIGNMENTS

RESULT 1

A12971
heparin-binding lectin - human (fragment)
C.Species: Homo sapiens (man)
C.Date: 12-Oct-1989 #sequence_revised 12 Oct 1989 #seq change 10 Feb 1990
C.Accession: A12971
R.Kohnke-Godt, R.; Gabius, H.J.
Biochemistry 28, 6531-6538, 1989
A.Title: Heparin-binding lectin from human placenta: purification and partial amino acid sequence
A.Reference number: A12971; MUID:9001207; PMID:285801
A.Accession: A12971
A.Status: preliminary
A.Molecule type: protein
A.Residues: 1-15 <KOH>
C.Keywords: heparin binding

Query Match 37.38; Score 11; DP 2; Length 15;
Best Local Similarity 41.78; Pred. NC. 38.02;
Matches 5; Conservative 4; Mismatches 1; Gaps 1

CV 3 swpspsvvyvzyyp 14

DB 1 ACPKATKVKVSP 12

RESULT 2

A27803
myosin light chain, smooth muscle - turkey (fragment)
C.Date: 05-Jun-1988 #sequence_revised 05 Jun 1988 #seq change 29 Sep-1990
C.Accession: A27803
P.Bergur, A.P.; Robinson, E.A.; Appella, E.; Sellers, J.R.
J. Biol. Chem. 263, 7633-7637, 1987
A.Title: Sequence of the sites phosphorylated by protein kinase C in the smooth muscle
A.Reference number: A27803; MUID:9001207; PMID:304411
A.Accession: A27803
A.Molecule type: protein
A.Residues: 1-16 <BEN>
C.Superfamily: calmodulin, calmodulin repeat, hemody
C.Keywords: EF hand, muscle, smooth muscle

Query Match 34.94; Score 29; DP 2; Length 16;
Best Local Similarity 38.51; Pred. NC. 34.42;
Matches 5; Conservative 4; Mismatches 1; Gaps 1

CV 2 SSESSESESESESE 14

DB 2 SPKATKVKVSP 14

RESULT 3

A28144

ribosomal protein S27a - bovine (fragment)
 C:Species: Bos primigenius taurus (cattle)
 C:Date: 29 Aug 1999 #sequence_revision 26 Aug 1999 #text_change 21 Jul 2000
 C:Accession: A28144
 R:RefSeq: X.L., Beckstead, M.
 J. Biol. Chem. 263, 4926-4931, 1988
 A:Title: Extended reading frame of a ubiquitin gene encodes a stable, conserved, basic P
 A:Reference number: A28144, MIP 4916043, EMBL 493412
 A:Accession: A28144
 A:Molecule type: Protein
 A:Residues: 1-16
 A:Residues: 1-16
 C:Keywords: Ubiquitin, ribosomal protein, stable, conserved, basic P

Query Match 32.7%, Score 29, DB 2, Length 16,
 Best Local Similarity 32.7%, Pred. No. 3.7e+01,
 Matches 5, Conservative 2, Mismatches 0, Indels 0, Gaps 0.

QY 7 SKKKKK 13

DE 1 AKKKKK 7

PF00174

C53275

Ig kappa chain J3 segment H95 allotype rabbit (fragment)

C:Species: Oryzopsis latipes (rice)

C:Date: 04 May 1994 #sequence_revision 19 Nov 1994 #text_change 16 Aug 1995

C:Accession: C53275

R:RefSeq: H. March, P.A.

Immunogenetics 34, 201-207, 1991

A:Title: Evolution of the rabbit immunoglobulin kappa chain genes.

A:Reference number: A23275, MIP 4916043, EMBL 493412

A:Accession: C53275

A:Molecule type: DNA

A:Residues: 1-13

A:Residues: 1-13

C:Keywords: Immunoglobulin, kappa chain

Query Match 32.7%, Score 29, DB 2, Length 13,

Best Local Similarity 32.7%, Pred. No. 3.7e+01,

Matches 5, Conservative 2, Mismatches 0, Indels 0, Gaps 0.

QY 2 SKKKKKKKKK 14

DE 1 STGGGTEHRE 12

RESULT 5

G45681

orf 61 1 - phage T6 (fragment)

C:Species: phage T6

C:Date: 20 Sep 1993 #sequence_revision 19 Nov 1994 #text_change 19 Nov 1994

C:Accession: G45681

R:RefSeq: H. March, P.A.

Immunogenetics 34, 201-207, 1991

A:Title: Analysis of five presumptive protein coding sequences clustered between the ph

A:Reference number: A45681, MIP 4916043, EMBL 493412

A:Accession: G45681

A:Molecule type: Nucleic acid

A:Residues: 1-16

A:Residues: 1-16

C:Keywords: Immunoglobulin, kappa chain

Query Match 30.1%, Score 25, DB 2, Length 16,

Best Local Similarity 30.1%, Pred. No. 3.7e+01,

Matches 5, Conservative 0, Mismatches 1, Indels 0, Gaps 0.

QY AKKKKK 13

DE 4 KKKKK 9

RESULT 6

PC4382

Lebittin 4.5K polypeptide - Soybean (fragment)

N:Alternate names: acid soluble 26K protein

C:Species: Glycine max

C:Date: 06 Nov 1997 #sequence_revision 06 Nov 1997 #text_change 18 Jul 2001

C:Accession: PC4382

R:RefSeq: V. Harada, K.

Plant Cell Physiol. 39, 1291-1297, 1998

A:Title: Purification and characterization of a 4.5 kDa polypeptide from

A:Reference number: PC4382, MIP 4916043, EMBL 493412

A:Accession: PC4382

A:Molecule type: Protein

A:Residues: 1-14

A:Residues: 1-14

C:Keywords: This protein is rich in hydrophilic amino acid, and highly heat stable.

Query Match 28.9%, Score 24, DB 2, Length 14,

Best Local Similarity 28.9%, Pred. No. 2.7e+01,

Matches 5, Conservative 1, Mismatches 2, Indels 0, Gaps 0.

QY 9 KKKKKKK 15

DE 3 KKKKKKK 10

RESULT 7

I19407

Placental calcium-binding protein, western wall mouse (fragment)

C:Species: Mus musculus (western wild mouse)

C:Date: 04 May 1994 #sequence_revision 19 Nov 1994 #text_change 20 Sep 1999

C:Accession: I19407

R:RefSeq: X. Harada, K.

Plant Cell Physiol. 39, 1291-1297, 1998

A:Title: Purification and characterization of a 4.5 kDa polypeptide from

A:Reference number: I19407, MIP 4916043, EMBL 493412

A:Accession: I19407

A:Molecule type: Protein

A:Residues: 1-15

A:Residues: 1-15

C:Keywords: This protein is rich in hydrophilic amino acid, and highly heat stable.

Query Match 28.9%, Score 24, DB 2, Length 15,

Best Local Similarity 28.9%, Pred. No. 2.7e+01,

Matches 5, Conservative 2, Mismatches 2, Indels 0, Gaps 0.

QY 6 PSKKKKKK 13

DE 8 PKKKKKKK 15

RESULT 8

S13903

Chaperone, TSP-related - rat

C:Species: Avicula caryophylla (oat)

C:Date: 04 May 1994 #sequence_revision 19 Nov 1994 #text_change 18 Jul 2001

C:Accession: S13903

R:RefSeq: V. Harada, K.

Plant Cell Physiol. 39, 1291-1297, 1998

A:Title: Purification and characterization of a 4.5 kDa polypeptide from

A:Reference number: S13903, MIP 4916043, EMBL 493412

A:Accession: S13903

A:Molecule type: Protein

A:Residues: 1-14

A:Residues: 1-14

C:Keywords: This protein is rich in hydrophilic amino acid, and highly heat stable.

Query Match 27.7%, Score 23, DB 2, Length 14,

Best Local Similarity 27.7%, Pred. No. 3.7e+01,

Matches 4, Conservative 1, Mismatches 2, Indels 0, Gaps 0.

Query Match 26.5%; Score 22; DB 2; Length 14;
Best Local Similarity 44.4%; Pred. No. 5, 10, 15;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 7 SKKPKK 15
| | | | |
DB 6 AKKSRKSG 14

RESULT 12
PC7076
Spectrin alpha chain, non-erythroid mouse fragment
N:Alternate names: fodrin alpha chain
C:Species: Mus musculus (house mouse)
C:Date: 18 Aug 1998 #sequence_revision 19-Aug-2000 #ext_change 19-Aug-2000
C:Accession: PC7076
R:Tsugita, A.; Kawakami, T.; Uchida, T.; Sakai, T.; Yama, M.; Maruta, T.; Watanabe, Y.
Electrophoresis 21, 1853-1871, 2000
A:Title: Proteome analysis of mouse brain: Two-dimensional electrophoretic profiles
A:Reference number: PC7072
A:Accession: PC7076
A:Molecule type: protein
A:Residues: 1-9 <TSU>
A:Experimental source: strain C57BL/6J; Sex: male; Brain, cortex
C:Keywords: brain

Query Match 25.3%; Score 21; DB 2; Length 9;
Best Local Similarity 57.1%; Pred. No. 2, 4, 6;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 5 SPSKPK 11
| | | | |
DB 2 SATPKK 8

RESULT 13
PQ0785
NADH2 dehydrogenase (EC 1.6.99.3) 27K chain - fava bean mitochondrial fragment
N:Alternate names: complex I 27K chain, NADH ubiquinone reductase 27K chain
C:Species: mitochondrial fava faba (fava bean)
C:Date: 03 May 1994 #sequence_revision 03-Jul-1994 #ext_change 03-Jun-2000
C:Accession: PQ0785
R:Letenne, S.; Boutry, M.
Plant Physiol 102, 435-443, 1993
A:Title: Purification and preliminary characterization of the mitochondrial complex I
A:Reference number: PQ0775; MUID:94151477; PMID:8104859
A:Accession: PQ0785
A:Molecule type: protein
A:Residues: 1-10 <LET>
C:Comment: Complex I, mitochondrial NADH ubiquinone reductase, is the first of the
ranging from 5K to 75K.
C:Genetics:
A:Genome: mitochondrion
C:Keywords: electron transfer; mitochondrial; oxidoreductase

Query Match 25.3%; Score 21; DB 2; Length 14;
Best Local Similarity 42.9%; Pred. No. 5, 10, 15;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 6 PSKPKK 12
| | | | |
DB 4 PGKPKK 10

RESULT 14
S71300
ICL3 protein - Paramecium tetraurelia (fragment)
C:Species: Paramecium tetraurelia
C:Date: 11-Mar-1998 #sequence_revision 17-Apr-1998 #ext_change 17-Dec-1998
C:Accession: S71300
R:Madodd, L.; Klotz, G.; Le Caer, J.F.; Boisson, J.
Eur. J. Biochem. 238, 121-129, 1996

Query Match 26.5%; Score 22; DB 2; Length 14;
Best Local Similarity 44.4%; Pred. No. 5, 10, 15;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 7 SKKPKK 15
| | | | |
DB 6 AKKSRKSG 14

RESULT 12
PC7076
Spectrin alpha chain, non-erythroid mouse fragment
N:Alternate names: fodrin alpha chain
C:Species: Mus musculus (house mouse)
C:Date: 18 Aug 1998 #sequence_revision 19-Aug-2000 #ext_change 19-Aug-2000
C:Accession: PC7076
R:Tsugita, A.; Kawakami, T.; Uchida, T.; Sakai, T.; Yama, M.; Maruta, T.; Watanabe, Y.
Electrophoresis 21, 1853-1871, 2000
A:Title: Proteome analysis of mouse brain: Two-dimensional electrophoretic profiles
A:Reference number: PC7072
A:Accession: PC7076
A:Molecule type: protein
A:Residues: 1-9 <TSU>
A:Experimental source: strain C57BL/6J; Sex: male; Brain, cortex
C:Keywords: brain

Query Match 25.3%; Score 21; DB 2; Length 9;
Best Local Similarity 57.1%; Pred. No. 2, 4, 6;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 5 SPSKPK 11
| | | | |
DB 2 SATPKK 8

RESULT 13
PQ0785
NADH2 dehydrogenase (EC 1.6.99.3) 27K chain - fava bean mitochondrial fragment
N:Alternate names: complex I 27K chain, NADH ubiquinone reductase 27K chain
C:Species: mitochondrial fava faba (fava bean)
C:Date: 03 May 1994 #sequence_revision 03-Jul-1994 #ext_change 03-Jun-2000
C:Accession: PQ0785
R:Letenne, S.; Boutry, M.
Plant Physiol 102, 435-443, 1993
A:Title: Purification and preliminary characterization of the mitochondrial complex I
A:Reference number: PQ0775; MUID:94151477; PMID:8104859
A:Accession: PQ0785
A:Molecule type: protein
A:Residues: 1-10 <LET>
C:Comment: Complex I, mitochondrial NADH ubiquinone reductase, is the first of the
ranging from 5K to 75K.
C:Genetics:
A:Genome: mitochondrion
C:Keywords: electron transfer; mitochondrial; oxidoreductase

Query Match 25.3%; Score 21; DB 2; Length 14;
Best Local Similarity 42.9%; Pred. No. 5, 10, 15;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 6 PSKPKK 12
| | | | |
DB 4 PGKPKK 10

RESULT 14
S71300
ICL3 protein - Paramecium tetraurelia (fragment)
C:Species: Paramecium tetraurelia
C:Date: 11-Mar-1998 #sequence_revision 17-Apr-1998 #ext_change 17-Dec-1998
C:Accession: S71300
R:Madodd, L.; Klotz, G.; Le Caer, J.F.; Boisson, J.
Eur. J. Biochem. 238, 121-129, 1996

Query Match 26.5%; Score 22; DB 2; Length 14;
Best Local Similarity 44.4%; Pred. No. 5, 10, 15;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 7 SKKPKK 15
| | | | |
DB 6 AKKSRKSG 14

RESULT 12
PC7076
Spectrin alpha chain, non-erythroid mouse fragment
N:Alternate names: fodrin alpha chain
C:Species: Mus musculus (house mouse)
C:Date: 18 Aug 1998 #sequence_revision 19-Aug-2000 #ext_change 19-Aug-2000
C:Accession: PC7076
R:Tsugita, A.; Kawakami, T.; Uchida, T.; Sakai, T.; Yama, M.; Maruta, T.; Watanabe, Y.
Electrophoresis 21, 1853-1871, 2000
A:Title: Proteome analysis of mouse brain: Two-dimensional electrophoretic profiles
A:Reference number: PC7072
A:Accession: PC7076
A:Molecule type: protein
A:Residues: 1-9 <TSU>
A:Experimental source: strain C57BL/6J; Sex: male; Brain, cortex
C:Keywords: brain

Query Match 25.3%; Score 21; DB 2; Length 9;
Best Local Similarity 57.1%; Pred. No. 2, 4, 6;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 5 SPSKPK 11
| | | | |
DB 2 SATPKK 8

RESULT 13
PQ0785
NADH2 dehydrogenase (EC 1.6.99.3) 27K chain - fava bean mitochondrial fragment
N:Alternate names: complex I 27K chain, NADH ubiquinone reductase 27K chain
C:Species: mitochondrial fava faba (fava bean)
C:Date: 03 May 1994 #sequence_revision 03-Jul-1994 #ext_change 03-Jun-2000
C:Accession: PQ0785
R:Letenne, S.; Boutry, M.
Plant Physiol 102, 435-443, 1993
A:Title: Purification and preliminary characterization of the mitochondrial complex I
A:Reference number: PQ0775; MUID:94151477; PMID:8104859
A:Accession: PQ0785
A:Molecule type: protein
A:Residues: 1-10 <LET>
C:Comment: Complex I, mitochondrial NADH ubiquinone reductase, is the first of the
ranging from 5K to 75K.
C:Genetics:
A:Genome: mitochondrion
C:Keywords: electron transfer; mitochondrial; oxidoreductase

Query Match 25.3%; Score 21; DB 2; Length 14;
Best Local Similarity 42.9%; Pred. No. 5, 10, 15;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 6 PSKPKK 12
| | | | |
DB 4 PGKPKK 10

RESULT 14
S71300
ICL3 protein - Paramecium tetraurelia (fragment)
C:Species: Paramecium tetraurelia
C:Date: 11-Mar-1998 #sequence_revision 17-Apr-1998 #ext_change 17-Dec-1998
C:Accession: S71300
R:Madodd, L.; Klotz, G.; Le Caer, J.F.; Boisson, J.
Eur. J. Biochem. 238, 121-129, 1996

Query Match 26.5%; Score 22; DB 2; Length 14;
Best Local Similarity 44.4%; Pred. No. 5, 10, 15;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 7 SKKPKK 15
| | | | |
DB 6 AKKSRKSG 14

RESULT 12
PC7076
Spectrin alpha chain, non-erythroid mouse fragment
N:Alternate names: fodrin alpha chain
C:Species: Mus musculus (house mouse)
C:Date: 18 Aug 1998 #sequence_revision 19-Aug-2000 #ext_change 19-Aug-2000
C:Accession: PC7076
R:Tsugita, A.; Kawakami, T.; Uchida, T.; Sakai, T.; Yama, M.; Maruta, T.; Watanabe, Y.
Electrophoresis 21, 1853-1871, 2000
A:Title: Proteome analysis of mouse brain: Two-dimensional electrophoretic profiles
A:Reference number: PC7072
A:Accession: PC7076
A:Molecule type: protein
A:Residues: 1-9 <TSU>
A:Experimental source: strain C57BL/6J; Sex: male; Brain, cortex
C:Keywords: brain

Query Match 25.3%; Score 21; DB 2; Length 9;
Best Local Similarity 57.1%; Pred. No. 2, 4, 6;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 5 SPSKPK 11
| | | | |
DB 2 SATPKK 8

RESULT 13
PQ0785
NADH2 dehydrogenase (EC 1.6.99.3) 27K chain - fava bean mitochondrial fragment
N:Alternate names: complex I 27K chain, NADH ubiquinone reductase 27K chain
C:Species: mitochondrial fava faba (fava bean)
C:Date: 03 May 1994 #sequence_revision 03-Jul-1994 #ext_change 03-Jun-2000
C:Accession: PQ0785
R:Letenne, S.; Boutry, M.
Plant Physiol 102, 435-443, 1993
A:Title: Purification and preliminary characterization of the mitochondrial complex I
A:Reference number: PQ0775; MUID:94151477; PMID:8104859
A:Accession: PQ0785
A:Molecule type: protein
A:Residues: 1-10 <LET>
C:Comment: Complex I, mitochondrial NADH ubiquinone reductase, is the first of the
ranging from 5K to 75K.
C:Genetics:
A:Genome: mitochondrion
C:Keywords: electron transfer; mitochondrial; oxidoreductase

Query Match 25.3%; Score 21; DB 2; Length 14;
Best Local Similarity 42.9%; Pred. No. 5, 10, 15;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 6 PSKPKK 12
| | | | |
DB 4 PGKPKK 10

RESULT 14
S71300
ICL3 protein - Paramecium tetraurelia (fragment)
C:Species: Paramecium tetraurelia
C:Date: 11-Mar-1998 #sequence_revision 17-Apr-1998 #ext_change 17-Dec-1998
C:Accession: S71300
R:Madodd, L.; Klotz, G.; Le Caer, J.F.; Boisson, J.
Eur. J. Biochem. 238, 121-129, 1996

RX MESTINE-03002017; PubMed:1450037;
 RA Hughes G.J., Frutiger S., Paquet N., Ravier F., Pasquali C.,
 RA Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,
 RA Hochstrasser D.F.;
 RI "Plasma protein map: an update by microsequencing";
 RL Electrophoresis 13:707-714(1992).
 CC : MICHIGAN:IN THE X-DEL THE DETERMINED PT OF THIS UNKNOWN
 CC PROTEIN IS: 5. ITS MW IS: 48 KDa
 DR SWISS 2DPAGE; P30022; HUMAN.
 FT NON-TER 1
 FT NON-TER 9
 SO SEQUENCE 9 AA, 525 MW, 5225PDAAS676447 CDS64;

Query Match 22.98; Score 19; DB 1; Length 9;
 Best Local Similarity 100.0%; Field No. 1.1e+057
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 PGD 16
 DB 4 PGD 6

Search completed: March 3, 2003, 06:42:08
 Job time : 7.66667 secs


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CC Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostei,
CC Mammalia, Eutheria, Primates, Catarrhini, Hominoidea, Homo
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
FX MEDLINE 9459301, EMBL 9241100;
RA Novotny W F, Maffei T, Mehra P L, Milner P G;
RT "Identification of novel hepatitis releasable proteins, as well as the
FT cytochrome c-like and electrophoretic, in human hepatitis plasma";
FX Afr J Lab Med 13:1798-1805(1993)
SQ SEQUENCE 15 AA, 1027 MW, C34R63787844AC GPC64;

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Best Local Similarity 46.2%; Pred No 14e03;
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QY 3 SESSSESESESESESE 15
DB 2 AKRERKWKGGES 14

RESULT 3
Q997C1 PRELIMINARY; PRT; 11 AA.
AC Q997C1
DT 01-JUN-2001 (TrEMBLrel. 17, Created;
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DE Coat protein (fragment)
OS East African cassava mosaic virus.
OC Viruses, SSRNA viruses, Geminiviridae, Begomovirus.
OX NCBI_TaxID=62079;
RN [1]
RP SEQUENCE FROM N.A.
FX MEDLINE 2116306, PubMed 1172108,
RA Pita J S, Pondong V N, Sargue A, Ojo Nape G W, Ogwal S,
RA Pauguet C M;
RT "Recombination, pseudorecombination and synergism of geminiviruses are
RT determinant keys to the epidemic of severe cassava mosaic disease in
RT Uganda.";
FX J Gen Virol 82:655-665(2001)
DP EMBL: AF220374; AAK24739.1;
FT NON TER 11
SQ SEQUENCE 11 AA, 1016 MW, 17110699AAAG174 GPC64;

Query Match 31.3%; Score 26; DB 10; Length 11;
Best Local Similarity 40.0%; Pred No 14e03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 12 KPGGD 16
DB 3 KPGGD 7

RESULT 4
Q997C2 PRELIMINARY; PRT; 13 AA.
AC Q997C2
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 13, Last annotation update)
DE Csa peptidase (fragment)
GN SCPA.
OS Streptococcus pyogenes
OC Bacteria, Firmicutes, Bacillus/Clostridium group, Lactobacillales;
OC Streptococcaceae; Streptococcus
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A
RA STRAIN-AFL;
FX MEDLINE 9036070, EMBL 1463050;
RA Berge A, Rasmussen M, Bjorck L;
RT "Identification of an insertion sequence located in a region encoding

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FT vitalence factors of streptococcus pyogenes.";
FX Infect Immun 66:3449-3453(1998);
DP EMBL: AF064546; AAK18768.1;
DR MEROPS; SC8.020; -;
FT NON TER 13
SQ SEQUENCE 13 AA, 1603 MW, 52424244VF703 GPC74;

Query Match 31.3%; Score 26; DB 0; Length 13;
Best Local Similarity 76.4%; Pred No 14e03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KKKKKKGGD 16
DB 2 KKKKKLFFD 10

RESULT 5
Q997D0 PRELIMINARY; PRT; 14 AA.
AC Q997D0
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE Allinase (EC 4.4.1.4) (fragment)
OS Allium cepa (onion).
OC Eukaryota; Viridiplantae; Streptophyta, Embryophyta, Tracheophyta;
OC Spermatophyta; Magnoliophyta, Liliiflorae, Asparagales, Alliaceae;
OC Allium.
OX NCBI_TaxID=4679;
RN [1]
RP SEQUENCE FROM N.A.
FX MEDLINE 2116306, PubMed 1172108,
RA Pita J S, Pondong V N, Sargue A, Ojo Nape G W, Ogwal S,
RA Pauguet C M;
RT "Recombination, pseudorecombination and synergism of geminiviruses are
RT determinant keys to the epidemic of severe cassava mosaic disease in
RT Uganda.";
FX J Gen Virol 82:655-665(2001)
DP EMBL: AF220374; AAK24739.1;
FT NON TER 14
SQ SEQUENCE 14 AA, 1573 MW, 23547038SE18307 GPC04;

Query Match 31.3%; Score 26; DB 10; Length 14;
Best Local Similarity 71.4%; Pred No 14e03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSKKSPS 7
DB 0 GSKKSPS 14

RESULT 6
Q997D5 PRELIMINARY; PRT; 15 AA.
AC Q997D5
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE Tumor necrosis factor alpha (fragment).
GN TNFA OR TNF-ALPHA.
OS Homo sapiens (human)
OC Eukaryota, Metazoa; Chordata, Vertebrata, Euteleostei;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA TISSUE=BLVD;
FX Schagdarsurenjin U, Glaeser C;
RT "Polymorphism in intron 3 of TNFA, transition A to G.";
FX Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA TISSUE=BLVD;
FX Schagdarsurenjin U, Glaeser C;

```

Query Match 30.1%; Score 26; DP 11; Length 16;
Best Local Similarity 55.6%; Pred. No. 1, 1e-03;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QV 4 PPSKRYK 12
| | | | |
DB 2 KNPMKPK 10

RESULT 9
Q62531 PRELIMINARY; PRT; 15 AA.
AC Q62531;
DT 01-JUN-1998 (TrEMBLrel. 06, Created;
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update;
DT 01-NOV-1996 (TrEMBLrel. 19, Last annotation update;
DE Placental calcium-binding protein 18A2; FHLA; WFS; protein
DE (Metastatic cell protein) (fragment);
GN MTS1;
OS Mus spretus (Western wild mouse);
OC Eukaryota; Metazoa; Chordata; Primates; Vertebrata; Eutheria; Rodentia;
OC Mammalia; Furberia; Rodentia; Sciurognathia; Muridae; Murinae; Mus;
OX NCBI_TaxID=10096;
RN [1]_TaxID=10096;
RF SEQUENCE FROM N.A.
RC STRAIN=SPRET/EI;
RX MEDLINE=94319082; PubMed=8043949;
RA KC W.S., Wang X., Jordon J.H., Hagen M.D., Takahashi N., Yasukari Y.,
RA Nadeau J.H.;
RT "Genetic mapping of 40 cDNA clones on the mouse genome by PCR";
RL Mamm. Genome 5:349-355(1994);
CC -1- SIMILARITY: TO OTHER EF-HAND CALCIUM BINDING PROTEINS. AND WIFE
CC SPECIFICALLY TO S-100/CARP LIKE PROTEINS.
DR EMBL; U05696; AAA61936.1; -;
KW Calcium-binding; Placenta;
FT NON TER 1 1
SQ SEQUENCE 15 AA; 1824 MW; 31BBEA5139B7741 CB064;

Query Match 28.9%; Score 24; DP 11; Length 16;
Best Local Similarity 50.0%; Pred. No. 1e-03;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QV 6 PPSKRYK 13
| | | | |
DB 8 PPSKRYK 15

RESULT 10
Q46291 PRELIMINARY; PRT; 14 AA.
AC Q46291;
DT 01-NOV-1996 (TrEMBLrel. 01, Created;
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update;
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update;
DE Ribosomal protein S19 (Plagmanto);
OS Canadian peach X phytoplasma;
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
OC Actinopterygii; Actinopterygii; Actinopterygii; Actinopterygii;
OX NCBI_TaxID=35778;
RN [1]_TaxID=35778;
RF SEQUENCE FROM N.A.
RC MEDLINE=94350902; PubMed=8071194;
RA Gundersen D.E., Lee I.M., Rehner S.A., Davis P.E., Kinscherry L.T.;
RT "Phylogeny of mycoplasma-like organisms (phytoplasmas): 1 basis for
PT their classification";
PL J. Bacteriol. 176:5244-5254(1994);
DR EMBL; L2712; AAA61936.1; -;
FT NON TER 1 1
SQ SEQUENCE 14 AA; 1712 MW; 4CC478B8BFFFE4A3 CB064;

Query Match 27.7%; Score 23; DP 21; Length 14;
Best Local Similarity 41.7%; Pred. No. 4.1e-03;

Query Match 30.1%; Score 26; DP 11; Length 16;
Best Local Similarity 55.6%; Pred. No. 1, 1e-03;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QV 4 PPSKRYK 12
| | | | |
DB 2 KNPMKPK 10

RESULT 9
Q62531 PRELIMINARY; PRT; 15 AA.
AC Q62531;
DT 01-JUN-1998 (TrEMBLrel. 06, Created;
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update;
DT 01-NOV-1996 (TrEMBLrel. 19, Last annotation update;
DE Placental calcium-binding protein 18A2; FHLA; WFS; protein
DE (Metastatic cell protein) (fragment);
GN MTS1;
OS Mus spretus (Western wild mouse);
OC Eukaryota; Metazoa; Chordata; Primates; Vertebrata; Eutheria; Rodentia;
OC Mammalia; Furberia; Rodentia; Sciurognathia; Muridae; Murinae; Mus;
OX NCBI_TaxID=10096;
RN [1]_TaxID=10096;
RF SEQUENCE FROM N.A.
RC STRAIN=SPRET/EI;
RX MEDLINE=94319082; PubMed=8043949;
RA KC W.S., Wang X., Jordon J.H., Hagen M.D., Takahashi N., Yasukari Y.,
RA Nadeau J.H.;
RT "Genetic mapping of 40 cDNA clones on the mouse genome by PCR";
RL Mamm. Genome 5:349-355(1994);
CC -1- SIMILARITY: TO OTHER EF-HAND CALCIUM BINDING PROTEINS. AND WIFE
CC SPECIFICALLY TO S-100/CARP LIKE PROTEINS.
DR EMBL; U05696; AAA61936.1; -;
KW Calcium-binding; Placenta;
FT NON TER 1 1
SQ SEQUENCE 15 AA; 1824 MW; 31BBEA5139B7741 CB064;

Query Match 28.9%; Score 24; DP 11; Length 16;
Best Local Similarity 50.0%; Pred. No. 1e-03;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QV 6 PPSKRYK 13
| | | | |
DB 8 PPSKRYK 15

RESULT 10
Q46291 PRELIMINARY; PRT; 14 AA.
AC Q46291;
DT 01-NOV-1996 (TrEMBLrel. 01, Created;
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update;
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update;
DE Ribosomal protein S19 (Plagmanto);
OS Canadian peach X phytoplasma;
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
OC Actinopterygii; Actinopterygii; Actinopterygii; Actinopterygii;
OX NCBI_TaxID=35778;
RN [1]_TaxID=35778;
RF SEQUENCE FROM N.A.
RC MEDLINE=94350902; PubMed=8071194;
RA Gundersen D.E., Lee I.M., Rehner S.A., Davis P.E., Kinscherry L.T.;
RT "Phylogeny of mycoplasma-like organisms (phytoplasmas): 1 basis for
PT their classification";
PL J. Bacteriol. 176:5244-5254(1994);
DR EMBL; L2712; AAA61936.1; -;
FT NON TER 1 1
SQ SEQUENCE 14 AA; 1712 MW; 4CC478B8BFFFE4A3 CB064;

Query Match 27.7%; Score 23; DP 21; Length 14;
Best Local Similarity 41.7%; Pred. No. 4.1e-03;

10. treated
11. list sequence
12. list sequence
13. list annotated

14. list sequence
15. list sequence
16. list annotated

17. list sequence
18. list sequence
19. list annotated
20. list annotated

21. list sequence
22. list sequence
23. list annotated
24. list annotated

25. list sequence
26. list sequence
27. list annotated
28. list annotated
29. list annotated
30. list annotated

31. list sequence
32. list sequence
33. list annotated
34. list annotated
35. list annotated
36. list annotated




```

AAE24220
ID   AAR44220 standard; Protein, 12 AA.
XX
AC   AAR44220;
XX
DT   18-NOV-1992 (first entry)
XX
DE   Fragment of tenascin related peptide.
XX
KW   Tenascin, related peptide, cell attachment, antibody, angiogenesis,
KW   tumour metastasis, solid matrix, prosthetic device, vascular graft,
KW   percutaneous device.
XX
PN   WC9207872-A.
XX
PD   14-MAY-1992.
XX
PF   29-OCT-1991; 91WO-0508018.
XX
PR   30-OCT-1990; 90US-050667.
XX
PR   29-OCT-1990; 90US-0505920.
XX
PA   (CALB-7) CALIFORNIA INST RESEARCH LAB RES
XX
PI   Boulder CO,
XX
WI   1992 1990 1991.
XX
XX   New tenascin related peptides modulate cell attachment to
PT   tenascin, useful in inhibition of tumour metastasis and
PT   angiogenesis
XX
PS   Disclosure; page 8; 60pp; English.
XX
XX   The peptide may form an 8 or 9 terminal fragment of the protein
XX   peptide of AAR44220, which is a tenascin related peptide. This
XX   peptide mimics the ability of tenascin to promote cell attachment
XX   to the peptide and antibodies raised to it can be used to modulate cell
XX   attachment to tenascin esp to inhibit tumour metastasis and
XX   angiogenesis. The peptide is preferably attached to a solid matrix, eg
XX   collagen, nitrocellulose, polystyrene, glass, synthetic resin, long chain
XX   polyacrylate or synthetic resin fibre. It is especially operatively linked
XX   to a solid matrix forming a prosthetic device, percutaneous device,
XX   vascular graft, etc. For topical admin, it is formulated in a
XX   solution, saline, gel, colloid, powder etc
XX
SQ   Sequence 12 AA;
      Query Match 48.2%; Score 40; DB 13; Length 12;
      Best Local Similarity 98.9%; E-Val 1.7;
      Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
      QY 9 KKKKKKKKK 16
      DB 3 KKKKKKKKK 11
      RESULT 11
      AAY90160
      ID   AAY90160 standard; peptide; 11 AA.
      XX
      AC   AAY90160;
      XX
      DT   21-SEP-2000 (first entry)
      XX
      DE   UPAR targeting sequence with spacers #10.
      XX
      KW   Ligand epitope, UPAR, adenine type plasminogen activator receptor,
      KW   adenovirus, hexon, hexon loop, hexon loop, peripheral artery disease,
      KW   recombinant adenovirus vector, tumour, metastasis, gene therapy, asthma,
      KW   percutaneous device, cell attachment, inhibition, primary B-cell,
      KW   obesity, neurodegenerative disease, infection, autoimmune disease, HIV,
      KW   cell death, fracture, tissue modified cells
XX
XX   Adenovirus SP.
XX
XX   WC900012718-A1.
XX
XX   09-MAR-2000.
XX
XX   27 AUG 1990; 89WO 1901524.
XX
XX   0-AUG-1990; 89WO 1901524.
XX
XX   (AVET ) AVENTIS PHARMA SA.
XX
XX   Vigne E, Dedieu J, Latta M, Yeh P, Porticaudet M;
XX   WPI; 2000 054443/22.
XX
XX   Urokinase type plasminogen activator receptor (UPAR) targeted
XX   adenovirus, hexon loop, hexon loop, hexon loop, hexon loop, hexon
XX   fiber, hexon loop, hexon loop, hexon loop, hexon loop, hexon
XX   restenosis
XX
XX   Claim 15, Page 69, 128pp, English.
XX
XX   This sequence represents a targeting sequence for UPAR, and is linked
XX   by linker. The invention relates to an adenovirus from which a
XX   linker of the hexon loop or HI loop is replaced with a binding
XX   peptide, or targeting sequence, flanked by connecting amino acid spacers,
XX   to functionally display its binding specificity at the capsid surface.
XX   The invention also relates to a recombinant adenovirus vector where a
XX   binding peptide, or targeting sequence, is connected to the C-terminus of
XX   the fiber by a connecting spacer, or linker, so as to functionally
XX   display its binding specificity at the capsid surface. The adenovirus or
XX   recombinant adenovirus vector can be used to preferentially express a
XX   gene in a target cell, especially a cell that expresses a UPAR. The
XX   targeted adenovirus vector is preferably modified with a heterologous gene
XX   encoding a gene for treatment of a tumour or restenosis. The targeted
XX   adenovirus vector is useful for gene therapy treatment of a disease, and
XX   for manufacturing a medicine used in gene therapy treatment of a disease.
XX   The virus can be used to inhibit tumour growth, cell proliferation,
XX   to treat proliferative diseases, to treat infectious diseases, asthma, HIV,
XX   neurodegenerative diseases, infection, autoimmune disease, asthma, HIV,
XX   cell death, and fracture. The virus are particularly targeted against a
XX   urokinase type plasminogen activator receptor (UPAR). The adenovirus
XX   are typically modified without adversely impacting productivity of the
XX   vectors.
XX
SQ   Sequence 11 AA;
      Query Match 45.0%; Score 19, DB 21; Length 11;
      Best Local Similarity 89.0%; E-Val 10.21;
      Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
      QY 7 SKKKKKKK 15
      DB 2 SKKKKKKK 10
      RESULT 12
      AAY90169
      ID   AAY90169 standard; peptide, 13 AA.
      XX
      AC   AAY90169;
      XX
      DT   21-SEP-2000 (first entry)
      XX
      DE   UPAR targeting sequence with spacers #19.
      XX
      KW   Ligand epitope, UPAR, adenine type plasminogen activator receptor,
      KW   adenovirus, hexon, hexon loop, hexon loop, hexon loop, hexon loop,
      KW   recombinant adenovirus vector, tumour, metastasis, gene therapy, asthma,
      KW   percutaneous device, cell attachment, inhibition, primary B-cell,
      KW   obesity, neurodegenerative disease, infection, autoimmune disease, HIV,
      KW   cell death, fracture, tissue modified cells

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CC Synthetic.
XX WO9802454-A2.
XX 27-JAN-1998
XX 08-JUL-1997; 97WO-BP03715.
XX 15-JUL-1998; 98GB-0014971.
XX (ADPP-) APPOTTECH PLC.
XX Dodd I, Mossakowska DEI, Smith RAG;
XX WPI, 1998-11054/10.
XX Derivatives of soluble polypeptide(s) related to low affinity
XX membrane binding groups - useful for treating complement-related and
XX thrombotic diseases, providing improved localisation at cellular
XX membranes
XX Claim 11, Page 70, 75pp, English.
XX The present peptide sequence represents a specifically claimed membrane
XX binding element. The invention relates to a soluble derivative (A) of a
XX soluble polypeptide (B), which comprises at least 2 heterologous
XX membrane binding elements (MEE) of low membrane affinity covalently
XX associated with (i) MBE interact, independently and with their dynamic
XX additivity, with components of cellular or artificial membranes treatable with
XX (i) itself, specifically inflammation or any other complement-related
XX infection, sepsis, rheumatoid arthritis and many others, including
XX application to inducing leukaemia and thrombotic disease, but also to
XX treat allergy, induce weight loss, to treat ischaemia or asthma and as
XX immune modulators for treating multiple sclerosis. (A) are administered
XX orally, topically, by injection or inhalation at 0.01-10 (preferably
XX 0.1-10) mg/kg/day.
XX Sequence 16 AA;
XX
XX Query Match. 47 3%, Score 30, PP 10, Length 16;
XX Best Local Similarity 77.8% Pred. NO. 32;
XX Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 6 PSKKKKKKP 14
XX | | | | |
XX Db 3 PKKKKKKSP 11
XX
XX RESULT 15
XX AAW45881
XX ID AAW45881 standard; peptide; 16 AA.
XX AC AAW45881;
XX AC AAW45881;
XX DT 30-JUN-1998 (first entry)
XX DE Peptide membrane binding element.
XX
XX Membrane binding element; thrombotic disease; inflammation;
XX complement-related disease; soluble peptide.
XX Synthetic.
XX WO9802454-A2.
XX 27-JAN-1998.
XX 08-JUL-1997; 97WO-BP03715.
XX 15-JUL-1998; 98GB-0014971
XX
XX PA (ADPP-) APPOTTECH PLC
XX PI Dodd I, Mossakowska DEI, Smith RAG;
XX PP WPI, 1998-11054/10.
XX PT Derivatives of soluble polypeptide(s) related to low affinity
XX membrane binding groups - useful for treating complement-related and
XX thrombotic diseases, providing improved localisation at cellular
XX membranes
XX Claim 11, Page 70, 75pp, English.
XX The present peptide sequence represents a specifically claimed membrane
XX binding element. The invention relates to a soluble derivative (A) of a
XX soluble polypeptide (B), which comprises at least 2 heterologous
XX membrane binding elements (MEE) of low membrane affinity covalently
XX associated with (i) MBE interact, independently and with their dynamic
XX additivity, with components of cellular or artificial membranes treatable with
XX (i) itself, specifically inflammation or any other complement-related
XX infection, sepsis, rheumatoid arthritis and many others, including
XX application to inducing leukaemia and thrombotic disease, but also to
XX treat allergy, induce weight loss, to treat ischaemia or asthma and as
XX immune modulators for treating multiple sclerosis. (A) are administered
XX orally, topically, by injection or inhalation at 0.01-10 (preferably
XX 0.1-10) mg/kg/day.
XX Sequence 16 AA;
XX
XX Query Match. 47 3%, Score 30, PP 10, Length 16;
XX Best Local Similarity 77.8% Pred. NO. 32;
XX Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 6 PSKKKKKKP 14
XX | | | | |
XX Db 3 PKKKKKKSP 11
XX
XX Search completed: March 3, 2003, 06:44:32
XX CPU time 47 secs

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Sequence 100, App

Sequence 100, App

Sequence 100, App

Sequence 100, App

Sequence 100, App

Sequence 100, App

Sequence 100, App

Sequence 100, App

Sequence 100, App

Sequence 100, App

Sequence 100, App

Sequence 100, App

Sequence 100, App

Sequence 100, App

Sequence 100, App

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Sequence 100, App

Sequence 100, App

Sequence 100, App

Sequence 100, App

Sequence 100, App

Sequence 100, App

Sequence 100, App

Sequence 100, App

Sequence 100, App

Sequence 100, App

Sequence 100, App

ALIGNMENTS

RESULT 1

Sequence 33, Application US/0910186A
Patent No. US2002092041A1
GENERAL INFORMATION:
APPLICANT: Wang, Zuo-Liang
APPLICANT: Song, Wen-Yuang
APPLICANT: Hubert, Scott
APPLICANT: Richter, Todd
TITLE OF INVENTION: Procedures and Materials for
TITLE OF INVENTION: Disease Resistance in Plants
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.13
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/0910186A
FILING DATE: 13-AUG-1997
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/PACKET NUMBER: 623,655-189570S
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/576-0300
TELEFAX: 415/576-0300
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear

```

1 MOLECULE TYPE: peptide
2 FEATURE:
3 NAME/KEY: Modified-site
4 LOCATION: 13
5 OTHER INFORMATION: /product: "OTHER"
6 OTHER INFORMATION: /note: "Xaa - Ile, Met, Thr, Asn, Lys,
7 OTHER INFORMATION: Ser or Arg"
8 FEATURE:
9 NAME/KEY: Modified-site
10 LOCATION: 14
11 OTHER INFORMATION: /product: "OTHER"
12 OTHER INFORMATION: /note: "Xaa - Cys, Arg, Ser or Gly"
13 US 09-214-913-38
14
15 Query Match 44 61; Score 37, DB 8, Length 14;
16 Best Local Similarity 87.5%; Filed No. 267
17 Matches 7; Conservative 6; Mismatches 1; Indels 0; Gaps 0
18
19 QY 5 PPKKKKKK 12
20 DB 2 PPKKKKKK 9
21
22 RESULT 2
23 US-10-119-714-7
24 Sequence 7, Application US/10119714
25 Patent No. US6001234567A1
26 GENERAL INFORMATION:
27 APPLICANT: PETIT, CHRISTINE
28 APPLICANT: COUSSE, YVES-CRISTIAN, MACIA
29 APPLICANT: HARDELIN, JEAN-PIERRE
30 APPLICANT: SARAILH, CATHERINE
31 APPLICANT: EUGON, GENEVIEVE
32 APPLICANT: LEGOUIC, RENAUD
33 APPLICANT: AETOUIN, OLIVIER
34 APPLICANT: MAZIE, JEAN-CLAUDE
35 TITLE OF INVENTION: THERAPEUTIC COMPOSITION COMPRISING FAL PROTEIN AND USE
36 TITLE OF INVENTION: OF THE FAL PROTEIN FOR THE TREATMENT OF FETAL, PERINATAL,
37 TITLE OF INVENTION: NEURAL AND DEEPAL INJURY
38 FILE REFERENCE: 0680-0151-OXPECT
39 CURRENT APPLICATION NUMBER: 03/10/119,714
40 PRIOR FILING DATE: 2002-04-11
41 PRIOR APPLICATION NUMBER: US/09/419,036
42 PRIOR FILING DATE: 1999-09-12
43 NUMBER OF SEQ ID NOS: 9
44 SOFTWARE: Pascalik Ver. 2.1
45 SEQ ID NO: 7
46 LENGTH: 16
47 TYPE: PRT
48 ORGANISM: Artificial Sequence
49 FEATURE:
50 OTHER INFORMATION: Description of Artificial Sequence: peptide
51 US-10-119-714-7
52
53 Query Match 42 21; Score 25, DB 12, Length 16;
54 Best Local Similarity 54.5%; Filed No. 72;
55 Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
56
57 QY 5 PPKKKKKK 16
58 DB 4 PPKKKKKK 14
59
60 RESULT 3
61 US-09-214-913-38
62 Sequence 7, Application US/09/419,036
63 Patent No. US6001234567A1
64 GENERAL INFORMATION:
65 APPLICANT: PETIT, CHRISTINE
66 APPLICANT: COUSSE, YVES-CRISTIAN, MACIA
67 TITLE OF INVENTION: THERAPEUTIC COMPOSITION COMPRISING FAL PROTEIN AND USE
68 TITLE OF INVENTION: OF THE FAL PROTEIN FOR THE TREATMENT OF FETAL, PERINATAL,
69 TITLE OF INVENTION: NEURAL AND DEEPAL INJURY
70 FILE REFERENCE: 0680-0151-OXPECT
71 CURRENT APPLICATION NUMBER: 03/10/119,714
72 PRIOR FILING DATE: 2002-04-11
73 PRIOR APPLICATION NUMBER: US/09/419,036
74 PRIOR FILING DATE: 1999-09-12
75 NUMBER OF SEQ ID NOS: 9
76 SOFTWARE: Pascalik Ver. 2.1
77 SEQ ID NO: 7
78 LENGTH: 16
79 TYPE: PRT
80 ORGANISM: Artificial Sequence
81 FEATURE:
82 OTHER INFORMATION: Description of Artificial Sequence: peptide
83 US-10-119-714-7
84
85 Query Match 42 21; Score 25, DB 12, Length 16;
86 Best Local Similarity 54.5%; Filed No. 72;
87 Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
88
89 QY 5 PPKKKKKK 16
90 DB 4 PPKKKKKK 14
91
92 RESULT 3
93 US-09-214-913-38
94 Sequence 7, Application US/09/419,036
95 Patent No. US6001234567A1
96 GENERAL INFORMATION:
97 APPLICANT: PETIT, CHRISTINE
98 APPLICANT: COUSSE, YVES-CRISTIAN, MACIA
99 TITLE OF INVENTION: THERAPEUTIC COMPOSITION COMPRISING FAL PROTEIN AND USE
100 TITLE OF INVENTION: OF THE FAL PROTEIN FOR THE TREATMENT OF FETAL, PERINATAL,
101 TITLE OF INVENTION: NEURAL AND DEEPAL INJURY
102 FILE REFERENCE: 0680-0151-OXPECT
103 CURRENT APPLICATION NUMBER: 03/10/119,714
104 PRIOR FILING DATE: 2002-04-11
105 PRIOR APPLICATION NUMBER: US/09/419,036
106 PRIOR FILING DATE: 1999-09-12
107 NUMBER OF SEQ ID NOS: 9
108 SOFTWARE: Pascalik Ver. 2.1
109 SEQ ID NO: 7
110 LENGTH: 16
111 TYPE: PRT
112 ORGANISM: Artificial Sequence
113 FEATURE:
114 OTHER INFORMATION: Description of Artificial Sequence: peptide
115 US-10-119-714-7

```

```

1 ADDRESS: Rodman, Gibson & Costigan
2 STREET: 1185 Avenue of the Americas
3 CITY: New York
4 STATE: New York
5 COUNTRY: USA
6 ZIP: 10036
7 COMPUTER READABLE FORM:
8 MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
9 COMPUTER: IBM PS/2
10 OPERATING SYSTEM: DOS
11 SOFTWARE: Word Perfect 6.1
12 CURRENT APPLICATION DATA:
13 APPLICATION NUMBER: US/09/419,036
14 FILING DATE: July 29, 1998
15 CLASSIFICATION: 424
16 PRIOR APPLICATION DATA:
17 APPLICATION NUMBER:
18 FILING DATE:
19 ATTORNEY/AGENT INFORMATION:
20 NAME: Costigan, James V.
21 REGISTRATION NUMBER: 25,649
22 REFERENCE/DOCKET NUMBER: 575-008
23 TELECOMMUNICATION INFORMATION:
24 TELEPHONE: (212) 202-8989
25 INFORMATION FOR SEQ ID NO. 1:
26 SEQUENCE CHARACTERISTICS:
27 LENGTH: 10 amino acids
28 TYPE: amino acid
29 TOPOLOGY: circular
30 US 09-214-913-38
31
32 Query Match 41 0%; Score 14, DB 10; Length 10;
33 Best Local Similarity 76.5%; Filed No. 64;
34 Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
35
36 QY 4 PPKKKKKK 13
37 DB 1 PPKKKKKK 10
38
39 RESULT 4
40 US-09-214-913-38
41 Sequence 44, Application US/09/419,036
42 Patent No. US6001234567A1
43 GENERAL INFORMATION:
44 APPLICANT: Smith, Louis C.
45 Sparrow, James T.
46 Hauer, Jochen
47 Mims, Martha P.
48 TITLE OF INVENTION: LIPOPHILIC PEPTIDES FOR
49 MACROMOLECULE DELIVERY
50 NUMBER OF SEQUENCES: 139
51 CORRESPONDENCE ADDRESS:
52 ADDRESSEE: Lynn A. Lyon
53 STREET: 633 West Fifth Street
54 CITY: Los Angeles
55 STATE: California
56 COUNTRY: U.S.A.
57 ZIP: 90071-2056
58 COMPUTER READABLE FORM:
59 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
60 storage
61 COMPUTER: IBM Compatible
62 OPERATING SYSTEM: IBM PC DOS 5.0
63 SOFTWARE: Word Perfect 6.1
64 CURRENT APPLICATION DATA:
65 APPLICATION NUMBER: US/09/419,036
66 FILING DATE: 10 Mar 2001
67 CLASSIFICATION: 424
68 PRIOR APPLICATION DATA:
69 APPLICATION NUMBER: US/09/419,036

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INFORMATION FOR SEQ ID NO: 100:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 100:
US-09-805-301-100
Query Match 41.8%; Score 14; IP 3; Length 12;
Best Local Similarity 70.8%; Pred. No. 45;
Matches 7; Conservative 0; Mismatches 3; Gaps 0;
CY 4 KPSGKPKKKK 13
DB 1 KKKKKKKKKK 10
RESULT 6
US-09-805-301-7
Sequence 7, Application US/09805301
Patent No. US20020173456A1
GENERAL INFORMATION:
APPLICANT: Smith, Louis C.
Sparrow, James T.
Hauer, Jochen
Mrs. Martha P.
TITLE OF INVENTION: LIPOPHILIC PEPTIDES FOR
NUMBER OF SEQUENCES: 139
CORRESPONDENCE ADDRESS:
ADDRESSEE: LYON & LYON
STREET: 633 West Fifth Street
Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 6.0
SOFTWARE: Word Perfect 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/805,301
FILING DATE: 12-Mar-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/594,041
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Warburton, Richard C.
REGISTRATION NUMBER: 32,127
REFERENCE/DOCKET NUMBER: 217/189
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1400
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-805-301-7
Query Match 41.8%; Score 14; IP 3; Length 12;
Best Local Similarity 70.8%; Pred. No. 45;
Matches 7; Conservative 0; Mismatches 3; Gaps 0;

UNKNOWN
EXACT NO.
Richard C.
Warburton, 32,127
REG. NO. 217/189
TELEPHONE: 213 489 1400
TELEFAX: 213 955 0440
TELEX: 67 3510
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 44:
US-09-805-301-44
Query Match 41.8%; Score 14; IP 3; Length 12;
Best Local Similarity 70.8%; Pred. No. 45;
Matches 7; Conservative 0; Mismatches 3; Gaps 0;
CY 4 KPSGKPKKKK 13
DB 1 KKKKKKKKKK 10
RESULT 6
US-09-805-301-7
Sequence 7, Application US/09805301
Patent No. US20020173456A1
GENERAL INFORMATION:
APPLICANT: Smith, Louis C.
Sparrow, James T.
Hauer, Jochen
Mrs. Martha P.
TITLE OF INVENTION: LIPOPHILIC PEPTIDES FOR
NUMBER OF SEQUENCES: 139
CORRESPONDENCE ADDRESS:
ADDRESSEE: LYON & LYON
STREET: 633 West Fifth Street
Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 6.0
SOFTWARE: Word Perfect 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/805,301
FILING DATE: 12-Mar-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/594,041
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Warburton, Richard C.
REGISTRATION NUMBER: 32,127
REFERENCE/DOCKET NUMBER: 217/189
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1400
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-805-301-7
Query Match 41.8%; Score 14; IP 3; Length 12;
Best Local Similarity 70.8%; Pred. No. 45;
Matches 7; Conservative 0; Mismatches 3; Gaps 0;

Cy 4 KSPSPKPKK 13
| | | | |
Db 1 KPPPKPKK 10

RESULT 7

US-09-805-301-45

Sequence 45, Application US/09805301

Patent No. US20020173456A1

GENERAL INFORMATION:

APPLICANT: Smith, Louis C.

Sparrow, James T.

Hauer, Jochen

Mims, Martha P.

TITLE OF INVENTION: LIPOPHILIC PEPTIDES FOR

MACROMOLECULE DELIVERY

NUMBER OF SEQUENCES: 139

CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon & Lyon

STREET: 633 West Fifth Street

Suite 4700

CITY: Los Angeles

STATE: California

COUNTRY: U.S.A.

ZIP: 90071 2066

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

COMPUTER: IBM Compatible

OPERATING SYSTEM: IBM P.C. DOS 6.0

SOFTWARE: Word Perfect 6.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/805,301

FILING DATE: 12 Mar 2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/584,043

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Warburg, Richard J.

REGISTRATION NUMBER: 32,327

REFERENCE: PCT NUMBER: 11/189

TELECOMMUNICATION INFORMATION:

TELEPHONE: (213) 489-1600

TELEFAX: (213) 955-0410

TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 45:

SEQUENCE CHARACTERISTICS:

LENGTH: 13 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

FEATURE:

OTHER INFORMATION: "Xaa" stands for any naturally

occurring amino acid and

analogues thereof.

SEQUENCE DESCRIPTION: SEQ ID NO: 45:

US-09-805-301-45

Query Match 41.0%; Score 34; DB 9; Length 13;

Best Local Similarity 70.0%; Pred. No. 80;

Matches 7; Conservative 0; Mismatches 2; Indels 2; Caps 0;

Cy 4 KSPSPKPKK 13
| | | | |
Db 1 KPPPKPKK 10

RESULT 9

US-09-805-301-101

Sequence 101, Application US/09805301

Patent No. US20020173456A1

GENERAL INFORMATION:

APPLICANT: Smith, Louis C.

Sparrow, James T.

Hauer, Jochen

Mims, Martha P.

TITLE OF INVENTION: LIPOPHILIC PEPTIDES FOR

MACROMOLECULE DELIVERY

NUMBER OF SEQUENCES: 139

CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon & Lyon

STREET: 633 West Fifth Street

Suite 4700

CITY: Los Angeles

STATE: California

COUNTRY: U.S.A.

ZIP: 90071 2066

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

COMPUTER: IBM Compatible

OPERATING SYSTEM: IBM P.C. DOS 6.0

SOFTWARE: Word Perfect 6.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/805,301

FILING DATE: 12 Mar 2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/584,043

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Warburg, Richard J.

REGISTRATION NUMBER: 32,327

REFERENCE: PCT NUMBER: 11/189

TELECOMMUNICATION INFORMATION:

TELEPHONE: (213) 489-1600

TELEFAX: (213) 955-0410

TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 101:

SEQUENCE CHARACTERISTICS:

LENGTH: 13 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

FEATURE:

SEQUENCE DESCRIPTION: SEQ ID NO: 101:

US-09-805-301-101

Query Match 41.0%; Score 34; DB 9; Length 13;

Best Local Similarity 70.0%; Pred. No. 80;

Matches 7; Conservative 0; Mismatches 2; Indels 2; Caps 0;

CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/584,043
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 12,127
REFERENCE/DOCKET NUMBER: 217,199
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 483-1677
TELEFAX: (213) 955-0442
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
OTHER INFORMATION: "Xaa" stands for any naturally
occurring amino acid and
analogues thereof.
SEQUENCE DESCRIPTION: SEQ ID NO: 46:
US-09-805-301-46
Query Match 41.0%; Score 34; DP 2; Length 14;
Best Local Similarity 70.0%; Pred. No. 96;
Matches 7; Conservative 0; Mismatches 3; Gaps 0;
QY 4 KPSKKKKKK 13
DP 1 KKKKKKKKK 10
RESULT 11
US-09-805-301-102
Sequence 102, Application US/09805101
Patent No. 622022179456A1
GENERAL INFORMATION:
APPLICANT: Smith, Louis C.
Sparrow, James T.
Hauer, Jochen
Wims, Martha D.
TITLE OF INVENTION: LIPIDIC PEPTIDES FOR
MACROMOLECULE DELIVERY
NUMBER OF SEQUENCES: 139
CORRESPONDENCE ADDRESS:
ADDRESSEE: LYON & LYON
STREET: 633 West Fifth Street
Suite 4720
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 MB
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 4.0
SOFTWARE: Word Perfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09805,101
FILING DATE: 12-Mar-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/584,043
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 12,127
REFERENCE/DOCKET NUMBER: 217,199
TELECOMMUNICATION INFORMATION:

US-09-805-301-102
Sequence 102, Application US/09805101
Patent No. 622022179456A1
GENERAL INFORMATION:
APPLICANT: Smith, Louis C.
Sparrow, James T.
Hauer, Jochen
Wims, Martha D.
TITLE OF INVENTION: LIPIDIC PEPTIDES FOR
MACROMOLECULE DELIVERY
NUMBER OF SEQUENCES: 139
CORRESPONDENCE ADDRESS:
ADDRESSEE: LYON & LYON
STREET: 633 West Fifth Street
Suite 4720
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 MB
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 4.0
SOFTWARE: Word Perfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09805,101
FILING DATE: 12-Mar-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/584,043
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 12,127
REFERENCE/DOCKET NUMBER: 217,199
TELECOMMUNICATION INFORMATION:

```

1 TELEPHONE (213) 499-1000
2 TELEFAX (213) 955-0440
3 TELEX 67-3510
4 INFORMATION FOR SEQ ID NO: 102:
5 SEQUENCE CHARACTERISTICS:
6 LENGTH: 14 amino acids
7 TYPE: amino acid
8 STRANDEDNESS: single
9 TOPOLOGY: linear
10 MOLECULE TYPE: peptide
11 SEQUENCE DESCRIPTION: SEQ ID NO: 102:
12
13 Query Match 41.0%, Score 34, Pos 16, Length 14,
14 Best Local Similarity 70.0%, Pos 8, 36,
15 Matches 7, Conservative 0, Mismatches 3, Indels 0, Gaps 0,
16
17 QY 4 YPSPPPPPPK 13
18 | | | | |
19 DB 1 KKKKKKKKK 10
20
21 RESULT 13
22 US-09-983-067-1
23 : Country 1, Applicant 1, Pct No 1, Date 1
24 : Patent No 1, Publication No 1, Date 1
25 : GENERAL INFORMATION:
26 APPLICANT: INOVA, APO
27 APPLICANT: SHIMIZU, Yoshiko
28 APPLICANT: CEDA, Tokyo
29 TITLE OF INVENTION: Processes for Producing Peptides By Using In Vitro
30 TITLE OF INVENTION: Transcription/Translation System
31 FILE REFERENCE: 1993-011P
32 CURRENT APPLICATION NUMBER: US/09/001,067
33 CURRENT FILING DATE: 2001-10-23
34 PRIOR APPLICATION NUMBER: JP 294765/2001
35 PRIOR FILING DATE: 2001-09-26
36 PRIOR APPLICATION NUMBER: JP 227094/2001
37 PRIOR FILING DATE: 2001-07-27
38 PRIOR APPLICATION NUMBER: JP 231726-1
39 PRIOR FILING DATE: 2001-01-15
40 PRIOR APPLICATION NUMBER: JP 401417/2000
41 PRIOR FILING DATE: 2000-12-28
42 NUMBER OF SEQ ID NOS: 6
43 SOFTWARE: PatentIn version 3.1
44 SEQ ID NO 1
45 LENGTH: 14
46 TYPE: PRT
47 ORGANISM: Bovine sp.
48 US-09-983-067-1
49
50 Query Match 41.0%, Score 34, Pos 16, Length 14,
51 Best Local Similarity 70.0%, Pos 8, 36,
52 Matches 7, Conservative 0, Mismatches 3, Indels 0, Gaps 0,
53
54 QY 4 YPSPPPPPPK 13
55 | | | | |
56 DB 5 QKKKKKKKK 14
57
58 RESULT 13
59 US-09-805-301-9
60 : Sequence 9, Application US/09805301
61 : Patent No US20020173456A1
62 : GENERAL INFORMATION:
63 APPLICANT: Smith, Louis C.
64 APPLICANT: Sparrow, James T.
65 APPLICANT: Hauer, Jochen
66 APPLICANT: Mims, Martha P.
67 TITLE OF INVENTION: LIPOPHILIC PEPTIDES FOR
68 MACROMOLECULE DELIVERY
69 NUMBER OF SEQUENCES: 139
70 CORRESPONDENCE ADDRESS:
71 ADDRESS: Lyon & Lyon
72 STREET: 411 West Fifth Street
73 CITY: Los Angeles
74 STATE: California
75 COUNTRY: U.S.A.
76 ZIP: 90071-2066
77 COMPUTER PEAPARIR FORM-
78 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
79 COMPUTER: IBM Compatible
80 OPERATING SYSTEM: IBM P.C. DOS 6.0
81 SOFTWARE: Word Perfect 6.1
82 OFF-WARE Word Perfect 6.1

```

```

1 SPONSOR: Lyon & Lyon
2 STREET: 411 West Fifth Street
3 CITY: Los Angeles
4 STATE: California
5 COUNTRY: U.S.A.
6 ZIP: 90071-2066
7 COMPUTER READABLE FORM:
8 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
9 COMPUTER: IBM Compatible
10 OPERATING SYSTEM: IBM P.C. DOS 6.0
11 SOFTWARE: Word Perfect 6.1
12 CURRENT APPLICATION DATA:
13 APPLICATION NUMBER: 09805301
14 FILING DATE: 12 May 2001
15 CLASSIFICATION: <Unknown>
16 PRIOR APPLICATION DATA:
17 APPLICATION NUMBER: 08/584,043
18 FILING DATE: <Unknown>
19 ATTORNEY/AGENT INFORMATION:
20 NAME: Warburg, Richard J.
21 REGISTRATION NUMBER: 93,327
22 REFERENCE/DOCKET NUMBER: 212/189
23 TELECOMMUNICATION INFORMATION:
24 TELEPHONE: (213) 499-1600
25 TELEFAX: (213) 955-0440
26 TELEX: 67-3510
27 INFORMATION FOR SEQ ID NO: 9:
28 SEQUENCE CHARACTERISTICS:
29 LENGTH: 14 amino acids
30 TYPE: amino acid
31 STRANDEDNESS: single
32 TOPOLOGY: linear
33 MOLECULE TYPE: peptide
34 SEQUENCE DESCRIPTION: SEQ ID NO: 9:
35
36 Query Match 41.0%, Score 34, Pos 16, Length 14,
37 Best Local Similarity 70.0%, Pos 8, 36,
38 Matches 7, Conservative 0, Mismatches 3, Indels 0, Gaps 0,
39
40 QY 4 YPSPPPPPPK 13
41 | | | | |
42 DB 1 KKKKKKKKK 10
43
44 RESULT 14
45 US-09-805-301-47
46 : Sequence 47, Application US/09805301
47 : Patent No. US20020173456A1
48 : GENERAL INFORMATION:
49 APPLICANT: Smith, Louis C.
50 APPLICANT: Sparrow, James T.
51 APPLICANT: Hauer, Jochen
52 APPLICANT: Mims, Martha P.
53 TITLE OF INVENTION: LIPOPHILIC PEPTIDES FOR
54 MACROMOLECULE DELIVERY
55 NUMBER OF SEQUENCES: 139
56 CORRESPONDENCE ADDRESS:
57 ADDRESS: Lyon & Lyon
58 STREET: 411 West Fifth Street
59 CITY: Los Angeles
60 STATE: California
61 COUNTRY: U.S.A.
62 ZIP: 90071-2066
63 COMPUTER PEAPARIR FORM-
64 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
65 COMPUTER: IBM Compatible
66 OPERATING SYSTEM: IBM P.C. DOS 6.0
67 SOFTWARE: Word Perfect 6.1

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DATA:
 REGISTRATION NUMBER: 12,327
 REPRESENTATIVE NUMBER: 217/197
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (213) 489-1600
 TELEFAX: (213) 955-0440
 TELEX: 67-3510
 INFORMATION FOR SEQ ID NO: 103:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 15 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 SEQUENCE DESCRIPTION: SEQ ID NO: 103:
 MS-09-005-301-103

Query Match 41.0% Score 34; DB 3; Length 15;
 Best Local Similarity 70.0% Pred. No. 91;
 Matches 7, Conservative 0, Mismatches 0; Indels 0; Gaps 0;

QV 4 KPSKPKKKKK 11
 DR 1 KKKKKKKKK 10

Search completed: March 3, 2003, 06:55:21
 Job time : 9 secs

DATA:
 REGISTRATION NUMBER: 12,327
 REPRESENTATIVE NUMBER: 217/197
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (213) 489-1600
 TELEFAX: (213) 955-0440
 TELEX: 67-3510
 INFORMATION FOR SEQ ID NO: 103:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 15 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 SEQUENCE DESCRIPTION: SEQ ID NO: 103:
 MS-09-005-301-103

Query Match 41.0% Score 34; DB 3; Length 15;
 Best Local Similarity 70.0% Pred. No. 91;
 Matches 7, Conservative 0, Mismatches 0; Indels 0; Gaps 0;

QV 4 KPSKPKKKKK 11
 DR 1 KKKKKKKKK 10

Search completed: March 3, 2003, 06:55:21
 Job time : 9 secs

DATA:
 REGISTRATION NUMBER: 12,327
 REPRESENTATIVE NUMBER: 217/197
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (213) 489-1600
 TELEFAX: (213) 955-0440
 TELEX: 67-3510
 INFORMATION FOR SEQ ID NO: 103:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 15 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 SEQUENCE DESCRIPTION: SEQ ID NO: 103:
 MS-09-005-301-103

Query Match 41.0% Score 34; DB 3; Length 15;
 Best Local Similarity 70.0% Pred. No. 91;
 Matches 7, Conservative 0, Mismatches 0; Indels 0; Gaps 0;

QV 4 KPSKPKKKKK 11
 DR 1 KKKKKKKKK 10

Search completed: March 3, 2003, 06:55:21
 Job time : 9 secs

DATA:
 REGISTRATION NUMBER: 12,327
 REPRESENTATIVE NUMBER: 217/197
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (213) 489-1600
 TELEFAX: (213) 955-0440
 TELEX: 67-3510
 INFORMATION FOR SEQ ID NO: 103:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 15 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 SEQUENCE DESCRIPTION: SEQ ID NO: 103:
 MS-09-005-301-103

Query Match 41.0% Score 34; DB 3; Length 15;
 Best Local Similarity 70.0% Pred. No. 91;
 Matches 7, Conservative 0, Mismatches 0; Indels 0; Gaps 0;

QV 4 KPSKPKKKKK 11
 DR 1 KKKKKKKKK 10

Search completed: March 3, 2003, 06:55:21
 Job time : 9 secs

DATA:
 REGISTRATION NUMBER: 12,327
 REPRESENTATIVE NUMBER: 217/197
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (213) 489-1600
 TELEFAX: (213) 955-0440
 TELEX: 67-3510
 INFORMATION FOR SEQ ID NO: 103:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 15 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 SEQUENCE DESCRIPTION: SEQ ID NO: 103:
 MS-09-005-301-103

Query Match 41.0% Score 34; DB 3; Length 15;
 Best Local Similarity 70.0% Pred. No. 91;
 Matches 7, Conservative 0, Mismatches 0; Indels 0; Gaps 0;

QV 4 KPSKPKKKKK 11
 DR 1 KKKKKKKKK 10

Search completed: March 3, 2003, 06:55:21
 Job time : 9 secs

DATA:
 REGISTRATION NUMBER: 12,327
 REPRESENTATIVE NUMBER: 217/197
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (213) 489-1600
 TELEFAX: (213) 955-0440
 TELEX: 67-3510
 INFORMATION FOR SEQ ID NO: 103:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 15 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 SEQUENCE DESCRIPTION: SEQ ID NO: 103:
 MS-09-005-301-103

Query Match 41.0% Score 34; DB 3; Length 15;
 Best Local Similarity 70.0% Pred. No. 91;
 Matches 7, Conservative 0, Mismatches 0; Indels 0; Gaps 0;

QV 4 KPSKPKKKKK 11
 DR 1 KKKKKKKKK 10

Search completed: March 3, 2003, 06:55:21
 Job time : 9 secs



ZIP: 92122
COMPUTER READABLE FORM.
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT AFFILIATION DATA: US/99/469,582
APPLICATION NUMBER: 05-JUN-1995
CLASSIFICATION: 530
PRIORITY DATA:
PRIORITY APPLICATION DATA:
PRIORITY APPLICATION NUMBER: US 92/071,013
FILING DATE: 23-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,812
REFERENCE/DOCKET NUMBER: P-LA 1550
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-8001
TELEFAX: (619) 535-8919
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-469-582 15

every Match	19.46	Score 36, LB 1, Length 12,
Best Local Similarity	23.93	Prod No 29,
Matches 7, Conservative	1, Mismatches	5, Indels

by
I 555P5CFFFE 13

by
I 666T5A5SFFX 13

RESULT 3
UL 00 195 004B
Sequence 9, Application US/09105004P
Patent No. 4701364
GENERAL INFORMATION:
APPLICANT: Pose, Keith
APPLICANT: Off. Ad. Rubin
TITLE OF INVENTION: RETRO-FLUORESCENT COMPOUNDS AND THEIR
PREPARATION BY SAFELINK ASSEMBLY
NUMBER OF INVENTION: 24
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS
ADDRESSEE: Cooley Godward Castro Huddleston & Tatum
STREET: 5 Palo Alto Square, 3000 El Camino Real
CITY: Palo Alto
STATE: California
COUNTRY: U.S.A.
ZIP: 94306
COMPUTER HEADLINE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/1200, 004E
FILING DATE: 31 AUG 1993
CLASSIFICATION: 421
PRICE APPLICATION DATA:
APPLICATION NUMBER: US 09/057,504
FILING DATE: 05-MAY-1993
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Neeraj, Richard L.
REGISTRATION NUMBER: 30,092
REFERENCE/AGENT NUMBER: A20 001/0205
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 957-5000
TELEFAX: (415) 957-0663

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1 TELPEY: 399615 C00199PA
2 INFORMATION FOR SEQ 10: NO
3 SEQUENCE CHARACTERISTICS:
4 LENGTH: 11 amino acids
5 TYPE: amino acid
6 TOPOLOGY: linear
7 MOLECULE TYPE: peptide
8 HYPOTHEetical: NO
9 FEATURE:
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11 LOCATION: 1
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39 LOCATION: 10
40 OTHER INFORMATION: LYS-CXL
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Best local Similarity	87.5%	Pred No. 33		
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27	9	KKKKKKK	15
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1  RESULT 4
2  US-09-105-904B-21
3  ? Sequence 21, Application US/06105004B
4  ? Patent No. 6001364
5  ?
6  ? GENERAL INFORMATION
7  ? APPLICANT: Moss, Keith
8  ? APPLICANT: Offord, Robin
9  ? TITLE OF INVENTION: RETROVIRAL VACCINE CONTAINING ANT. THEIR
10 ? NUMBER OF INVENTION: PREPARATION BY PARALLEL ASSEMBLY
11 ? NUMBER OF SEQUENCES: 24
12 ? CORRESPONDENCE ADDRESS:
13 ? ADDRESS: 64141 Orchard Center, Highland & Tatum
14 ? STREET: 6 Palo Alto Square, 3800 El Camino Real
15 ? CITY: Palo Alto
16 ? STATE: California
17 ? COUNTRY: U. S. A.
18 ? ZIP: 94306
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20 ? COMMENTARY READABLE FORM:
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24 ? SOFTWARE: Patent In Release #1.0, Version #1.25

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1 TITLE OF INVENTION: METHOD OF INTRACELLULAR BINDING OF
2 TITLE OF INVENTION: PROTEINS
3 NUMBER OF SEQUENCES: 76
4 CORRESPONDENCE ADDRESS:
5 ADDRESSEE: DAVID G. CUSHMAN, EYE, BRONSTEIN, ROBERTS &
6 ADDRESSEE: CUSHMAN
7 STREET: 130 WATER STREET
8 CITY: BOSTON
9 STATE: MASSACHUSETTS
10 COUNTRY: US
11 ZIP: 02109
12 COMPUTER READABLE FORM:
13 MEDIUM TYPE: floppy disk
14 COMPILE: IBM PC compatible
15 OPERATING SYSTEM: PC-DOS/MS-DOS
16 SOFTWARE: Patent in Release #1.0, Version #1.25
17 CURRENT APPLICATION DATA:
18 APPLICATION NUMBER: US/89/438,145A
19 FILING DATE:
20 CLASSIFICATION: 435
21 ATTORNEY/AGENT INFORMATION:
22 NAME: EISENSTEIN, RONALD I.
23 REGISTRATION NUMBER: 30628
24 REFERENCE/DOCKET NUMBER: 41356
25 TELECOMMUNICATION INFORMATION:
26 TELEPHONE: (617) 523-1400
27 TELEFAX: (617) 523-6440
28 TELECOMMUNICATIONS TYPE: 00
29 INFORMATION FOR SEQUENCE CHARACTERISTICS:
30 SEQUENCE CHARACTERISTICS:
31 LENGTH: 10 amino acids
32 TYPE: amino acid
33 TOPOLOGY: linear
34 US-89-438-145A-54
35 Entry No. 41356, Sheet 4, of 4 Length 10,
36 Best Local Similarity 56.7%, Seed Match 42,
37 Matched 61, Substitution 2, Mismatch 1, Indels 0

38 20 5 0000000000 10
39 30 1 0000000000 9
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41 RESULT 12
42 US-89-287-145A-54
43 Sequence 54, Application US/89287145A
44 Patent No. 89/0236
45 GENERAL INFORMATION:
46 APPLICANT: MARASCO, WAYNE
47 APPLICANT: HASELTINE, WILLIAM
48 TITLE OF INVENTION: METHOD OF INTRACELLULAR BINDING OF
49 NUMBER OF SEQUENCES: 76
50 CORRESPONDENCE ADDRESS:
51 ADDRESSEE: DAVID G. CUSHMAN, EYE, BRONSTEIN, ROBERTS &
52 ADDRESSEE: CUSHMAN
53 STREET: 130 WATER STREET
54 CITY: BOSTON
55 STATE: MASSACHUSETTS
56 COUNTRY: US
57 ZIP: 02109
58 COMPUTER READABLE FORM:
59 MEDIUM TYPE: floppy disk
60 COMPUTER: IBM PC compatible
61 OPERATING SYSTEM: PC-DOS/MS-DOS
62 SOFTWARE: Patent in Release #1.0, Version #1.25
63 CURRENT APPLICATION DATA:
64 APPLICATION NUMBER: US/89/287,145A
65 FILING DATE:
66 CLASSIFICATION:
67 PRIOR APPLICATION DATA:
68 APPLICATION NUMBER: US/89/438,145A

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1      BILLING DATE:
2      ATTORNEY/AGENT INFORMATION:
3      NAME: HIGENSTEIN, RONALD I.
4      REGISTRATION NUMBER: 30628
5      REFERENCE: PET N°PER 41746
6      TELECOMMUNICATION INFORMATION:
7      TELEPHONE: (617) 523-3400
8      TELEFAX: (617) 523-6440
9      REMARKS: 200291 STRE UP
1     INFORMATION FOR SEQ ID NO: 54:
11    SEQUENCE CHARACTERISTICS:
12        LENGTH: 10 amino acids
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16 US-09-287-145A-54
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18 Query Match          41.0%   Score 34; DB 4; Length 10;
19 Exp. Ident. Similarity 57.1%   Ident. No. 12;
20 Matches 6; Conservative 0; Mismatches 4; Indels 0;
21
22 E SPQPPPPYK 13
23 | |||||
24 I TPTPTPTT 9
25
26 RESULT 13
27 US-09-208-966-45
28 Sequence 48 Application No. 966-45
29 Patent No. 6229173
30 GENERAL INFORMATION:
31 APPLICANT: Dowdy, Steven F.
32 TITLE OF INVENTION: AMT; PATERNIN SYSTEM AND METHODS OF USE THEREOF
33 FILE REFERENCE: 48481/1742
34 CURRENT APPLICATION NUMBER: 09/006,966
35 CURRENT FILING DATE: 1998-12-10
36 EARLIER APPLICATION NUMBER: 08/042,400
37 EARLIER FILING DATE: 1998-04-20
38 EARLIER APPLICATION NUMBER: 08/042,400
39 EARLIER FILING DATE: 1997-12-10
40 NUMBER OF SEQ IDS NOS: 57
41 SOFTWARE: Patentin Ver. 2.0
42 SEQ ID NO 45
43 LENGTH: 10
44 TYPE: PRT
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46 us-09-208-966-45
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52 E SPQPPPPYK 13
53 | |||||
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56 RESULT 14
57 US-09-556-111-14
58 Sequence 54; Application No. 09/006,966
59 Patent No. 6229173
60 GENERAL INFORMATION:
61 APPLICANT: MASAROG, WAYNE
62 TITLE OF INVENTION: METHOD OF INTERCELLULAR BINDING OF PROTEINS
63 NUMBER OF REFERENCES: 78
64 CORRESPONDENCE ADDRESS:
65 ADDRESSEE: DASHMAN, JEROME, AVE, NEWTON, MASSACHUSETTS 0
66 STREET: 130 WATER STREET
67 CITY: BOSTON
68 STATE: MASSACHUSETTS
69 COUNTRY: US

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 3. Strandedness: single
 4. Topology: linear
 5. Molecule type: peptide
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 Db 2 KSPSPKPKK 11

Search completed: March 3, 2003, 06:44:21
 Job time : 16.6667 secs

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 9. Other information: /label= Ac-
 10. Name/Key: Peptide
 11. Location: 11
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41.08

BLAST/MS-DOS
 Version #1.0, Vers: n #1.0

1. Length: 11, amino acids
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 11. Location: 11
 12. Other information: /label= -NH2
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 Matches 7; Mismatches 0; Gaps 0;

BLAST/MS-DOS
 Version #1.0, Vers: n #1.0

41.08

1. Length: 11, amino acids
 2. Type: AMINO ACID
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 6. Feature:
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 8. Location: 1
 9. Other information: /label= Ac-
 10. Name/Key: Peptide
 11. Location: 11
 12. Other information: /label= -NH2
 US-07-694-983-15
 Query Match
 Best Local Similarity 41.08; Score 34; DP 1; Length 11;
 Matches 7; Mismatches 0; Gaps 0;

41.08



Sequence version 5.1.1
1993-2003 Copyright 1993

usnstr sw model

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(without alignments)
4154:54 in cell updates/sec

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1993-2003

1993-2003

1993-2003
1993-2003
1993-2003

of results produced by change to have a
equal to the score of the result being printed,
times of the total in the distribution.

SUMMARIES

DB ID	Description
A61220	epsilon receptor m
P00684	photosystem I 15.9
A11416	ribosomal protein
A00115	photosystem I chal
A24344	ribosomal protein
A06150	photosystem I chal
A06185	nitrophorin 3 - ph
A06185	cytochrome c oxidase
A06185	hypothetical prote
A06185	transcription fact
A06185	DNA binding protei
A06185	platelet-derived u
A06185	hyaluronidase (EC
A06185	ribosomal protein
A06185	neurotrophin 3
A06185	ribosomal protein
A06185	gene p10 protein -
A06185	leberin 1 isoform
A06185	agrin - electric r
A06185	neuropeptide calla
A06185	proteinase inhibit
A06185	steroid receptor c
A06185	myosin light chain
A06185	histone H2B (clone
A06185	photosystem I chal
A06185	histone H2B - huma
A06185	spectrin alpha cha
A06185	ribosomal protein

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31	22	21-2	15	2	A43144	epsilon chain alpha
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33	22	21-2	16	2	A00115	photosystem I chal
34	22	21-2	16	2	C02292	photosystem I chal
35	22	21-2	16	2	C02292	photosystem I chal
36	22	21-2	19	2	B46592	photosystem I chal
37	22	21-2	20	2	B46592	photosystem I chal
38	22	21-2	20	2	A00115	photosystem I chal
39	22	21-2	20	2	C02292	photosystem I chal
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41	22	21-2	20	2	A00115	photosystem I chal
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44	21	20-2	11	2	S23373	photosystem I chal
45	21	20-2	13	2	S19413	photosystem I chal

ALIGNMENTS

RESULT 1
A61220
epsilon receptor modulating protein (EP 3.4.21.1) - mouse frame
C:Species: Mus musculus (house mouse)
C:Date: 19 May 1994 #sequence revision 19 May 1994 #seq. frame 21 Mar 1994
C:Accession: A61220
R:Matsumoto, S.; Katz, D.H.
Cell Immunol. 137, 252-259, 1991
A:Title: The murine epsilon receptor modulating protein: a novel serine protease with
A:Reference number: A61220; MUID:9158573; PMID:189941
A:Accession: A61220
A:Molecule type: protein
A:Residues: 1-18 <MAT>
C:Comment: This serine protease from a T cell hybridoma has not been fully
C:Keywords: hydrolase, serine protease

Query Match 29.8% Score 30; BB 21; Length 147
Best Local Similarity 57.1%; Pred. No. 5; Seq. 2;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 1;

Oy 7 PKK-KKKPKSKK 19
DB 5 PKKPKKKKKKKK 18

RESULT 2
P00684
Photosystem I 15.9 (P680) - Chlamydomonas reinhardtii fragment
C:Species: Chlamydomonas reinhardtii (Chlamydomonas reinhardtii)
C:Date: 19 May 1994 #sequence revision 19 May 1994 #seq. frame 19 Mar 1994
C:Accession: P00684
P:Okada, S.; Mikami, K.; Hayashida, N.; Nakamura, M.; Shimada, M.
Plant Physiol. 102, 1950-1957, 1993
A:Title: Wavelength-dependent phosphorylation of photosystem I
A:Reference number: P00684; MUID:9415345; PMID:144444
A:Accession: P00684
A:Molecule type: protein
A:Residues: 1-20 <P60>
C:Keywords: chlorophyll, photosynthesis, photosystem I, chlorophyll

Query Match 29.8% Score 30; BB 21; Length 217
Best Local Similarity 50.0%; Pred. No. 5; Seq. 2;
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Oy 3 SNETPKKKKKK 14
DB 3 SGLTKPKKKK 14

RESULT 3
S11416
ribosomal protein L6, cytosolic (unpublished) - rat fibroblast

A:Accession: B59326

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-20 <OBP>

A>Note: amino terminal of the mature form

C:Keywords: mitochondrion; protein biosynthesis; ribosome

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Best Local Similarity 55.63; Pred. No. 4.1e+03;

Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 6 TPKKKKKK 14

DB 8 SPKIKKPK 16

RESULT 15

239305

neurotoxin Tx3 - spider (Phoneutria nigriventer) (fragment)

C:Species: Phoneutria nigriventer

C>Date: 14-Feb-1992 #sequence_revision 14-Feb-1992 #text_change 07-Feb-1997

C:Accession: C39305

Ribeiro Jr., L.; Cordeiro, M.N.; Oliveira, E.B.; Diniz, C.R.

Toxicol 29, 1225-1233, 1991

A>Title: Isolation of neurotoxic peptides from the venom of the 'armed' spider Phoneutria

A:Reference number: A39305; MIM-9216603, PM10-1801316

A:Accession: C39305

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-19 <PEZ>

C:Keywords: neurotoxin

Query Match 22.63; Score 31.5; DB 2; Length 19;

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Matches 6; Conservative 4; Mismatches 4; Indels 1; Gaps 1;

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DB 6 NES-QKPNVYKKE 19

Search completed: March 3, 2003, 06:59:52

Job time : 48 secs


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2A Teshar S., O'Connell R.C., Bellock V.P., Korn L., Davies S.A.,
3A Veenstra J.A., Dow J.A.T.;
4T "Isolation and characterization of a leucine-rich like peptide of
5T Protophila melanogaster";
6L J. Exp. Biol. 202:3667-3676(1999).
7L [2]
8P SEQUENCE FROM N.A.
9C STRAIN-Berkeley;
10C Gelinker S.F., Aghayani A., Arcania T.T., Baxter E., Blazek P.G.,
11C Butenhoff C., Champe M., Chavez C., Chew M., Cieciolka L., Doyle C.M.,
12C Farfan D.F., Gallego P., George P.A., Harris N.L., Hoskins P.A.,
13C Heston J.A., Hernandez C.F., Karpis P., Kautsky J., Kir E., Lee B.,
14C Lewis S., Li P., Lomakin M.A., Mada R., Mochly R., Mochly Y.,
15C Nixson K., Paralek J.M., Park S., Pfeiffer P., Poon L., Queiroz A.,
16C Sethi H., Shih E., Swirski P.E., Wan E.H., Weinberg T., Zhang P.,
17C Cichon L.L., Fokin G.M.;
18C Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases
19C - FUNCTION: ACTS THROUGH INTRACELLULAR CALCIUM IN MAMMARIAN TUBULE
20C - CELL: STELLATE CELLS TO PAUSE CHLORIDE CONCENTRATION
21C
22C This SWISS-Prot entry is a fragment. It is provided through a collaboration
23C between the Swiss Institute of Bioinformatics and the EMBL Outstation
24C at the European Bioinformatics Institute. There are no restrictions on the
25C use by non-profit institutions as long as its content is in no way
26C modified and this statement is not removed. Usage by third parties for
27C commercial purposes requires a license agreement. (see http://www.isb.ch/submit/)
28C or send an email to license@isb.ch.
29C
30C EMBL: A00447, 1 P, 1 AMP TATCAGCG
31C FlyBase: FBgn003418; LocusLink:
32C NeuroPeptide; Amidation
33C W05583
34C AMIDATION
35C
36C SEQUENCE 10 AA, 143 MW, 4.91kDa, 10.1kDa, 10.1kDa
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OC      Bacteria; Firmicutes; Mollicutes; Achlepiasmatales;
OC      Achlepiasmataceae; Achlepiasma.
OX      NCBI TaxID=2148;
RN      [1]
RP      SEQUENCE FROM N.A. PubMed:156679;
RX      WFLINE 0216666, PubMed:156679;
RA      Lim P.O., Sears B.B.;
RT      "Evolutionary relationships of a plant-pathogenic mycoplasma-like
RT      organism and Achlepiasma laidlawii deduced from two ribosomal protein
RT      gene sequences."
RL      J. Bacteriol. 174:2606-2611(1992).
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CC      LOCATED AT THE A SITE OF THE PEPTIDYLTRANSFERASE CENTER
CC      (BY SIMILARITY).
CC      -!- SIMILARITY: BELONGS TO THE L15P FAMILY OF RIBOSOMAL PROTEINS.
CC      This SWISS-PROT entry is copyright. It is published through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use by non-profit institutions as long as its content is in no way
CC      modified and this statement is not removed. Usage by and for commercial
CC      entities requires a license agreement (see http://www.1st-sib.ch/announcement/
CC      or send an email to license@sib-sib.ch)
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DR      EMBL; M74771; AAC21914.1; -
DR      PIR; F41839;
DR      InterPro; IPR001114; Ribosomal_L15P.
DR      PROSITE; PS00566; RIBOSOMAL_L15P; PARTIAL.
DR      PROSITE; PS00731; RIBOSOMAL_L15P; PARTIAL.
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DB      4 PKRTYR 10

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Search completed: March 3, 2003, 06:56:38
Job time : 31 secs


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RX MEDLINE=92279243; PubMed=1317578;
RA Bukh J., Purcell R.H., Miller R.H.;
RT "Sequence analysis of the 5' noncoding region of hepatitis C virus."
RL Proc. Natl. Acad. Sci. U.S.A. 89:4942-4946(1992).
DR EMBL; M44830; AAA45700.1; -.
DP InterPro; IPR002502; HCV capsid.
DR Pfam; PF01543; HCV capsid; 1.
FT NON TER 13 13
SQ SEQUENCE 13 AA; 1512 MW; 454F97E1A42F76A3 E064;

Query Match 27.9%; Score 29; DB 12; Length 13;
Best Local Similarity 45.5%; Pred. No. 7.5e+02;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 3 SNETPRKPKYK 13
DB 3 TNPAPQPKTP 13

RESULT 9
Q81789 PRELIMINARY; PRT; 13 AA.
AC O81789;
DT 01-NOV-1996 (TrEMBLrel. 01, Created);
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update);
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update);
DE POLYPROTEIN (Fragment);
GN POLYPROTEIN.
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage, Flaviviridae;
OC Hepacivirus.
OX NCBI_TaxID=11103;
RN [1];
RP SEQUENCE FROM N.A.
RC STRAIN=DK11;
RX MEDLINE=92279243; PubMed=1317578;
RA Bukh J., Purcell R.H., Miller R.H.;
RT "Sequence analysis of the 5' noncoding region of hepatitis C virus."
RL Proc. Natl. Acad. Sci. U.S.A. 89:4942-4946(1992).
DR EMBL; M44831; AAA45706.1; -.
DP InterPro; IPR002502; HCV capsid.
DR Pfam; PF01543; HCV capsid; 1.
FT NON TER 13 13
SQ SEQUENCE 13 AA; 1512 MW; 454F97E1A42F76A3 E064;

Query Match 27.9%; Score 29; DB 12; Length 13;
Best Local Similarity 45.5%; Pred. No. 7.5e+02;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 3 SNETPRKPKYK 13
DB 3 TNPAPQPKTP 13

RESULT 10
Q81791 PRELIMINARY; PRT; 13 AA.
AC O81791;
DT 01-NOV-1996 (TrEMBLrel. 01, Created);
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update);
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update);
DE POLYPROTEIN (Fragment);
GN POLYPROTEIN.
OS Hepatitis C virus.
OC Viruses; ssRNA positive strand viruses, no DNA stage, Flaviviridae;
OC Hepacivirus.
OX NCBI_TaxID=11103;
RN [1];
RP SEQUENCE FROM N.A.
RC STRAIN=DK13;
RX MEDLINE=92279243; PubMed=1317578;
RA Bukh J., Purcell R.H., Miller R.H.;
```

RT "Sequence analysis of the 5' noncoding region of hepatitis C virus."
 PL Procl. Natl. Acad. Sci. U.S.A. 99:4942-4946(1992)
 DR EMBL; M84832; AAA45693.1; -
 DR InterPro; IPR002522; HCV_capsid.
 DR Pfam; PF01543; HCV_capsid; 1.
 FI NCBI RefSeq; NC_001522; HCV_capsid; 1.
 SC SEQUENCE 13 AA, 1572 MW, 4645721A42FC763 CRC64;

Query Match 27.9%; Score 29; DB 12; Length 13;
 Best local similarity 45.5%; Pred. No. 7.5e+02;
 Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 3 SNETPKPKKKYK 13
 DB 3 TNPKPQKTKR 13

RESULT 11

ID Q81772 PRELIMINARY; PRT; 13 AA.
 AC Q81772;
 DT 01-NOV-1996 (TRENBLREL 01, Created;
 DT 01-NOV-1996 (TRENBLREL 01, Last sequence update)
 DT 01-DEC-2001 (TRENBLREL 19, Last annotation update)
 DE Polypeptide (Fragment).
 GN POLYPROTEIN.
 OS Hepatitis C virus.
 OC Viruses; ssRNA positive strand viruses, no DNA stage, Flaviviridae;
 OC Hepacivirus.
 OC NCBI_TaxID 11103;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-S9;
 PY MEDLINE 92279243; PubMed 1317579;
 RA Bukh J., Purcell R.H., Miller R.H.;
 RT "Sequence analysis of the 5' noncoding region of hepatitis C virus."
 RL Proc. Natl. Acad. Sci. U.S.A. 89:4942-4946(1992)
 DR EMBL; M84833; AAA45690.1; -
 DR InterPro; IPR002522; HCV_capsid.
 DR Pfam; PF01543; HCV_capsid; 1.
 FI NCBI RefSeq; NC_001522; HCV_capsid; 1.
 SC SEQUENCE 13 AA, 1572 MW, 4645721A42FC762 CRC64;

Query Match 27.9%; Score 29; DB 12; Length 13;
 Best local similarity 45.5%; Pred. No. 7.5e+02;
 Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 3 SNETPKPKKKYK 13
 DB 3 TNPKPQKTKR 13

RESULT 12

ID Q81760 PRELIMINARY; PRT; 13 AA.
 AC Q81760;
 DT 01-NOV-1996 (TRENBLREL 01, Created;
 DT 01-NOV-1996 (TRENBLREL 01, Last sequence update)
 DT 01-DEC-2001 (TRENBLREL 19, Last annotation update)
 DE Polypeptide (Fragment).
 GN POLYPROTEIN.
 OS Hepatitis C virus.
 OC Viruses; ssRNA positive strand viruses, no DNA stage, Flaviviridae;
 OC Hepacivirus.
 OC NCBI_TaxID 11103;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-S9;
 PY MEDLINE 92279243; PubMed 1317579;
 RA Bukh J., Purcell R.H., Miller R.H.;
 RT "Sequence analysis of the 5' noncoding region of hepatitis C virus."
 RL Proc. Natl. Acad. Sci. U.S.A. 89:4942-4946(1992)
 DR EMBL; M84836; AAA45697.1; -

IS InterPro; IPR002522; HCV_capsid.
 PL Pfam; PF01543; HCV_capsid; 1.
 DR EMBL; M84832; AAA45693.1; -
 DR InterPro; IPR002522; HCV_capsid.
 DR Pfam; PF01543; HCV_capsid; 1.
 FI NCBI RefSeq; NC_001522; HCV_capsid; 1.
 SC SEQUENCE 13 AA, 1572 MW, 4645721A42FC763 CRC64;

Query Match 27.9%; Score 29; DB 12; Length 13;
 Best local similarity 45.5%; Pred. No. 7.5e+02;
 Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 3 SNETPKPKKKYK 13
 DB 3 TNPKPQKTKR 13

RESULT 13

ID Q81773 PRELIMINARY; PRT; 13 AA.
 AC Q81773;
 DT 01-NOV-1996 (TRENBLREL 01, Created;
 DT 01-NOV-1996 (TRENBLREL 01, Last sequence update)
 DT 01-DEC-2001 (TRENBLREL 19, Last annotation update)
 DE Polypeptide (Fragment).
 GN POLYPROTEIN.
 OS Hepatitis C virus.
 OC Viruses; ssRNA positive strand viruses, no DNA stage, Flaviviridae;
 OC Hepacivirus.
 OC NCBI_TaxID 11103;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-S9;
 PY MEDLINE 92279243; PubMed 1317579;
 RA Bukh J., Purcell R.H., Miller R.H.;
 RT "Sequence analysis of the 5' noncoding region of hepatitis C virus."
 RL Proc. Natl. Acad. Sci. U.S.A. 89:4942-4946(1992)
 DR EMBL; M84838; AAA45691.1; -
 DR InterPro; IPR002522; HCV_capsid.
 DR Pfam; PF01543; HCV_capsid; 1.
 FI NCBI RefSeq; NC_001522; HCV_capsid; 1.
 SC SEQUENCE 13 AA, 1572 MW, 4645721A42FC763 CRC64;

Query Match 27.9%; Score 29; DB 12; Length 13;
 Best local similarity 45.5%; Pred. No. 7.5e+02;
 Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 3 SNETPKPKKKYK 13
 DB 3 TNPKPQKTKR 13

RESULT 14

ID Q81763 PRELIMINARY; PRT; 13 AA.
 AC Q81763;
 DT 01-NOV-1996 (TRENBLREL 01, Created;
 DT 01-NOV-1996 (TRENBLREL 01, Last sequence update)
 DT 01-DEC-2001 (TRENBLREL 19, Last annotation update)
 DE Polypeptide (Fragment).
 GN POLYPROTEIN.
 OS Hepatitis C virus.
 OC Viruses; ssRNA positive strand viruses, no DNA stage, Flaviviridae;
 OC Hepacivirus.
 OC NCBI_TaxID 11103;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-S9;
 PY MEDLINE 92279243; PubMed 1317579;
 RA Bukh J., Purcell R.H., Miller R.H.;
 RT "Sequence analysis of the 5' noncoding region of hepatitis C virus."
 RL Proc. Natl. Acad. Sci. U.S.A. 89:4942-4946(1992)
 DR EMBL; M84839; AAA45691.1; -
 DR InterPro; IPR002522; HCV_capsid.
 DR Pfam; PF01543; HCV_capsid; 1.
 FI NCBI RefSeq; NC_001522; HCV_capsid; 1.
 SC SEQUENCE 13 AA, 1572 MW, 4645721A42FC763 CRC64;

QY 3 SNETPKPKKKYK 13
 DB 3 TNPKPQKTKR 13

W: 4649751A42F772A F 64;
S: Score 29; DP 13; Length 13;
M: Pred. No. 7; Labels 0; Gaps 0;

W: 4649751A42F772A F 64;
S: Score 29; DP 13; Length 13;
M: Pred. No. 7; Labels 0; Gaps 0;

W: 4649751A42F772A F 64;
S: Score 29; DP 13; Length 13;
M: Pred. No. 7; Labels 0; Gaps 0;

W: 4649751A42F772A F 64;
S: Score 29; DP 13; Length 13;
M: Pred. No. 7; Labels 0; Gaps 0;

W: 4649751A42F772A F 64;
S: Score 29; DP 13; Length 13;
M: Pred. No. 7; Labels 0; Gaps 0;

W: 4649751A42F772A F 64;
S: Score 29; DP 13; Length 13;
M: Pred. No. 7; Labels 0; Gaps 0;



11	44	42.3	15	23	AB581217	Anti-bacterial mem
12	44	42.3	17	19	AAW45880	Peptide membrane b
13	44	42.3	17	21	AAW58862	Membrane binding e
14	40	38.5	15	22	AAW58862	Human diacylglycer
15	40	38.5	18	22	AAW58862	Human diacylglycer
16	40	38.5	19	15	AAW45197	MAWKS data muta
17	39	37.5	19	18	AAW19823	Universal transfer
18	39	36.5	14	23	AAW73329	Human protease in
19	38	36.5	16	19	AAW45880	Peptide membrane b
20	38	36.5	15	21	AAW58862	Membrane binding e
21	38	36.5	16	23	ABW1347	Anti-bacterial mem
22	38	36.5	17	19	AAW45880	Peptide membrane b
23	38	36.5	17	21	AAW58862	Membrane binding e
24	37.5	36.1	15	20	AAW45880	Covalently modify
25	37.5	36.1	18	20	AAW45880	Peptide membrane b
26	37.5	36.1	18	22	AAW45880	Human nuclear pro
27	37	35.6	8	23	ABW4289	Anti-bacterial mem
28	37	35.6	10	18	AAW21612	Peptide membrane b
29	37	35.6	10	21	AAW58862	Peptide membrane b
30	37	35.6	16	19	AAW45880	Peptide membrane b
31	37	35.6	16	20	AAW73329	Fragment of human
32	37	35.6	16	21	AAW58862	Membrane binding e
33	37	35.6	16	23	ABW1347	Anti-bacterial mem
34	37	35.6	17	19	AAW45880	Myosin V/collectin
35	37	35.6	17	19	AAW45880	Peptide membrane b
36	37	35.6	17	21	AAW58862	Peptide membrane b
37	37	35.6	17	21	AAW26818	Membrane binding e
38	37	35.6	17	21	AAW58862	Membrane binding e
39	37	35.6	17	23	ABW1347	Anti-bacterial mem
40	37	35.6	17	23	ABW1347	Amino acid seque
41	37	35.6	18	22	AAW58862	Human polyphosph
42	37	35.6	18	22	AAW58862	MAWKS data muta
43	37	35.6	20	23	AAW58862	Label without prote
44	37	35.6	20	23	AAW58862	Label without prote
45	36	34.6	10	15	AAW45880	SV40 nuclear mem

ALIGNMENTS

RESULT 1
AAW45880
ID AAW45880 standard; peptide; 20 AA.
XX AC AAW45880;
XX DT 30-JUN-1998 (first entry)
DE Peptide membrane binding element.
XX KW Membrane binding element; thrombotic disease; inflammatory;
XX OS complement related disease; soluble peptide.
XX Synthetic.
XX EN W09802454-A2.
XX PD 22-JAN-1998.
XX PF 08-JUL-1997; 97WO-EP03715.
XX ER 15-JUL-1996; 96B-0014871.
XX PA (ADPP-) ADPPOTECH PLC.
XX PI Dodd I, Mossakowska DEI, Smith RAJ;
XX US WPI; 1994-11654/10.
XX ER Derivatives of soluble poly-peptide A. Labeled to low affinity
XX PT membrane binding groups - useful for treating complement related and
XX PT thrombotic diseases, providing improved localization of cellular
XX PT membranes

SUMMARIES

EP ID	Description
11	AAW45880
12	AAW58862
13	ABW1219
14	AAW42478
15	AAW58862
16	AAW71784
17	AAW21612
18	AAW58862
19	AAW45880
20	AAW58862

1. All results predicted to have a
2. All results predicted to have a
3. All results predicted to have a
4. All results predicted to have a
5. All results predicted to have a
6. All results predicted to have a
7. All results predicted to have a
8. All results predicted to have a
9. All results predicted to have a
10. All results predicted to have a

XX PS Claim 11; Page 39, 39pp, English.

XX CC The present peptide sequence represents a specifically tailored membrane

XX CC binding element, the invention relates to a suitable derivative (A) of a

XX CC suitable polypeptide (B), which comprises at least 1 heptapeptide

XX CC membrane binding element (MBE) of low membrane affinity, equivalently

XX CC associated with (1) MBE insert, independently and with thermodynamic

XX CC activity, with components of cellular or artificial membranes exposed

XX CC to extracellular fluids. (A) are used to treat disorders treatable with

XX CC (1) itself, specifically inflammation or any other complement-related

XX CC disorder such as rheumatoid disease, graft rejection, myocardial

XX CC infarction, sepsis, rheumatoid arthritis and many others; including

XX CC administration of blocking devices and therapeutic devices that also

XX CC treat allergy, induce weight loss, prevent infection, assist cell

XX CC immune modulation for treating multiple sclerosis. (A) are administered

XX CC orally, topically, by injection or inhalation at 0.01 to 10 (preferably

XX CC 0.1 to 5) mg/kg/day.

XX PS Sequence 20 AA;

Query Match 100.00, Score 104, BB 19, Length 20;

Best Local Similarity 100.00; Pred No 1 to 08;

Matches 20; Conservation 0; Mismatches 0; Index 0; Gap 0

QY 1 SPSTHTFFFFFFFFPKWG 20

Qb 1 SPSTHTFFFFFFFFPKWG 20

RESULT 2

AAV59857

QY 1 AAV59857 standard; Peptide, 20 AA.

XX AC AAV59857;

XX DT 08-MAY-2000 (first entry)

XX DE Membrane binding element used in anti-angiogenic polypeptide

XX KW Anti-angiogenic, angiogenesis inhibitor, membrane binding element;

XX KW cancer, tumor, therapy.

XX OS Synthetic.

XX PN W020000444 A1

XX PD 27-JAN-2000.

XX PF 16-JUL-1999; 99WO-GB012262.

XX PP 16-JUL-1999; 99GB 001505.

XX PA (ADPR-) ADPROTECH PLC.

XX PI Smith PAC, Raleigh NC, Stewart M, Cox VP,

XX PR WPI; 2000-02-03/16.

XX PS Claim 11; Page 32, 36pp, English.

XX CC The present polypeptide is a claimed derivative of a lysine-rich polypeptide

XX CC membrane binding element (MBE) that can be utilised in novel

XX CC membrane derivatives of anti-angiogenic polypeptides for the

XX CC invention. It comprises at least heptapeptides MBEs with low

XX CC membrane affinity that are equivalently attached to a soluble

XX CC anti-angiogenic polypeptide such as a non-catalytic region of human

XX CC plasminogen, fragments of related proteins containing kringle

XX CC domains, fragments of collagen or fibrin, neutralising

XX CC activated distinct receptors for angiogenic mediators, and

XX CC antagonists of integrins involved in angiogenesis. The MBEs

XX CC interact preferentially with thermodynamic activity, with

XX CC components of the vascular endothelium. (A) provide targeted

XX CC delivery of the anti-angiogenic polypeptide to the vascular endothelium,

XX CC sites of active angiogenesis, further reducing the vascular endothelium,

XX CC and therefore increase the local concentration and reduce the risk

XX CC of adverse effects on normal processes elsewhere in the vasculature.

XX CC They are used in a claimed method of treatment of primary or

XX CC secondary tumour.

XX PS Sequence 20 AA;

Query Match 100.00, Score 104, BB 21, Length 20;

Best Local Similarity 100.00; Pred No 1 to 08;

Matches 20; Conservation 0; Mismatches 0; Index 0; Gap 0

QY 1 SPSTHTFFFFFFFFPKWG 20

Qb 1 SPSTHTFFFFFFFFPKWG 20

RESULT 3

AAV59857

QY 1 ABB81239 standard; peptide, 20 AA.

XX AC ABB81239;

XX DT 20-AUG-2002 (first entry)

XX DE Antibacterial membrane binding peptide SEQ ID NO:6.

XX KW Antibiotic, glycopeptide, lipopeptide, anti-infective element;

XX KW bacterial infection, bacteriostatic, lipid-glycyl-kinophos inhibition;

XX KW antibiotic.

XX OS Synthetic.

XX PN W020000442 A1.

XX PD 10-MAY-2002.

XX PF 02-NOV-2001; 2001WO-GB04867.

XX PP 04-NOV-2001; 2000P-0004924.

XX PA (UNCA-) UNIV CAMBRIDGE TECH SERVICES LTD.

XX PI (ADPR-) ADPROTECH LTD.

XX PI Cooper VA, Parley JR;

XX PR WPI; 2002-04/492/50.

XX PS Antibacterial compound, useful for the treatment of a bacterial

XX PT infection by high gram positive or negative bacteria, comprises a

XX PT conjugate of glycopeptide and peptide membrane association element

XX PS Claim 1, Page 37, 64pp, English.

XX CC The present invention relates to an antibacterial compound comprising

XX CC a conjugate of glycopeptide and peptide membrane-association element

XX CC (1) comprises the formula V (W), where V is a glycopeptide moiety that

XX CC inhibits peptidoglycan biosynthesis in bacteria, W is a linking group;

XX CC W is a peptide membrane-association element, and X is H or a membrane

XX CC insertive element. Also described: (1) a method of treating or preventing

XX CC a bacterial infection, comprising the administration of (1); and (2) use

XX CC of (1) in the manufacture of a medicament for the treatment or prevention

XX CC of a bacterial infection. (1) are used in the manufacture of a medicament

XX CC for the treatment or prevention of a bacterial infection in a human or

XX CC animal, including the use of the conjugate and gram-negative bacteria

XX CC including *Yersinia* sp., *Escherichia* sp., *Pseudomonas* sp., *Staphylococcus* sp., *Vibrio* sp., *Neisseria* sp., *Klebsiella*

XX CC sp., *Haemophilus* sp., *Moraxella* sp., *Legionella* sp., *Acinetobacter* sp.,

RESULT 6

AAR71783

ID AAR71783 standard; peptide; 10 AA

XX

XX

AC AAR71783;

XX

DT 01-OCT-1995 (first entry)

XX

CE Peptide neutralising toxicity of Lipid A.

XX

KW Endotoxin; Lipid A; septic shock; lipopolysaccharide.

XX

OS Synthetic

XX

PN WO9203327-A.

XX

PD 02-FEB-1995.

XX

PF 21-JUL-1994; 94WO-EP02413.

XX

PY 26-JUL-1993; same as WO9203327.

XX

PA (BIOS-) BIOSYNTH SRL.

XX

PI Porro M;

XX

DN WPI; 1995-07-01/03.

XX

XX New peptide(s) for neutralising LPS endotoxin - comprising
 PT repeating units of a basic amino acid or basic and hydrophobic
 PT amino acids

XX

XX Claim 14, Page 21, 26pp, English.

XX

XX New peptides are claimed which are linear or cyclic peptides which
 CC include units of formula (A)n, where A is the cationic amino acid lys
 CC or Arg and n is 7 to 10, (A)n/m, where A is Lys or Arg, B is the hydrophobic
 CC amino acid Val, Leu, Ile, Tyr, Phe or Trp, and m is 3 or greater; and
 CC (ABC)p, where A is Lys or Arg, B and C are Val, Leu, Ile, Tyr, Phe or
 CC Trp, and p is 2 or greater.

XX The peptides bind to Lipid A of endotoxins and do not exhibit haemolytic
 CC activity. Hence they can be used therapeutically to treat septic shock
 CC and also in vitro to detoxify vaccines, drug solutions, injectable
 CC nutrient solutions, etc.

XX The present sequence is a specifically claimed example of the new
 CC peptides.

XX

SQ Sequence 10 AA;

XX

Query Match 42.3%; Score 44; DB 16; Length 10;

XX

Res: 1; 100 Similarity; 80.0%; Pred. No. 4.4;

XX

Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

XX

DY 9 KKKKKKKKKK 17

XX

DB 1 KKKKKKKKKK 10

XX

RESULT 7

AAW21600

ID AAW21600 standard; peptide; 10 AA.

XX

XX

AC AAW21600;

XX

DT 26-AUG-1997 (first entry)

XX

DE Antibiotic potentiating peptide #10.

XX

XX Potentiates antibiotic; microbial infection; lipopolysaccharide.

XX

KW Penicillin; outer bacterial membrane

XX

OS Synthetic

XX

PN WO9638163-A1.

XX

PD 05-DEC-1996.

XX

PF 24-MAY-1996; 96WO-EP02313.

XX

PE 31-MAY 1995; 95US-0455112.

XX

PA (BIOS-) BIOSYNTH SRL.

XX

PI Porro M; Varra M;

XX

DN WPI; 1997-03-04/03.

XX

XX Potentiating activity of antibiotic with peptide containing cationic
 PT amino acid sequence - reduces dose of antibiotic required

XX

XX Claim 16; Page 25; 37pp; English.

XX

XX The sequences given in AAW21599-613 represent peptides which act to
 CC potentiate the activity of an antibiotic when they are administered
 CC with the antibiotic. Compositions containing these peptides are used
 CC to treat or prevent microbial infections. These peptides bind to
 CC lipopolysaccharide on the bacteria or may increase permeability of
 CC the outer bacterial membrane to the antibiotic, allowing a reduction
 CC in the dose of antibiotic required by 10-90% of the normal dose for
 CC in vivo or in vitro application. Any toxic side effects are
 CC correspondingly reduced.

XX

XX Sequence 10 AA;

XX

Query Match 42.3%; Score 44; DB 16; Length 10;

XX

Res: 1; 100 Similarity; 80.0%; Pred. No. 4.4;

XX

Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

XX

DY 9 KKKKKKKKKK 17

XX

DB 1 KKKKKKKKKK 10

XX

RESULT 8

AAW56912

ID AAW56912 standard; peptide; 10 AA.

XX

XX

AC AAW56912;

XX

DT 14-APR-2000 (first entry)

XX

DE Peptide contained in a vaccine for bacterial infection.

XX

KW Vaccine; gram-negative infection; endotoxin; lipopolysaccharide; cyclic

XX

OS Synthetic.

XX

PN EP976402-A2.

XX

PD 02-FEB-2000.

XX

PF 27-JUL-1999; 99EP-0202476.

XX

PR 29-JUL-1998; 98US-0124280.

XX

PA (BIOS-) BIOSYNTH SRL.

XX

PI Porro M;

XX

DN WPI; 2000-12-04/12.

XX

XX New vaccine for prevention of gram-negative bacterial infections and
 PT endotoxin related disorders, comprising complex of peptide and LPS

52

[illegible]

18; score 44; 22 22; 10; 10;

of 4.4

Mismatches	Indels	Gaps
0	0	0

$\frac{1}{2} \times 6 = 3$

3

[illegible]

1. The metabolic disorders of the liver:

Final Report

polyepitope: binds to low affinity
useful for treating complement-related
with improved results at cellular

一、
 二、
 三、
 四、
 五、
 六、
 七、
 八、
 九、
 十、

tion represents a significant, shared cellular mechanism that relates to a metabolic derivative (A) of a set of substrates that are metabolically interconvertible. The effect of the derivative (A) on the rate of cellular growth is a function of the concentration of A, and the effect of A on the rate of cellular growth is a function of the concentration of A. The effect of A on the rate of cellular growth is a function of the concentration of A, and the effect of A on the rate of cellular growth is a function of the concentration of A.

to extraocular fluids. (A) are used to treat disorders treatable with (A) itself, specifically inflammation or any other inflammatory reaction (e.g. neurological diseases, graft rejection, myocardial infarction, sepsis, rheumatoid arthritis and many others, including application to the following diseases and therapies). (A) can also be used therapeutically, in those cases, to treat autoimmune diseases and immune modulators for treating multiple sclerosis. A pharmaceutical formulation, typically, by injection or inhalation at a dose of preferably 0.1 to 10 mg/kg/day.

AA	Sequence	16 AA;
SU		

$$M_1 + E_{M_1} \leq \frac{1}{2} \log \frac{1}{\epsilon}$$

42-157-10587-10588-10589-10590-10591-10592-10593-10594-10595-10596-10597-10598-10599-10600-10601-10602-10603-10604-10605-10606-10607-10608-10609-10610-10611-10612-10613-10614-10615-10616-10617-10618-10619-10620-10621-10622-10623-10624-10625-10626-10627-10628-10629-10630-10631-10632-10633-10634-10635-10636-10637-10638-10639-10640-10641-10642-10643-10644-10645-10646-10647-10648-10649-10650-10651-10652-10653-10654-10655-10656-10657-10658-10659-10660-10661-10662-10663-10664-10665-10666-10667-10668-10669-10670-10671-10672-10673-10674-10675-10676-10677-10678-10679-10680-10681-10682-10683-10684-10685-10686-10687-10688-10689-10690-10691-10692-10693-10694-10695-10696-10697-10698-10699-10700-10701-10702-10703-10704-10705-10706-10707-10708-10709-10710-10711-10712-10713-10714-10715-10716-10717-10718-10719-10720-10721-10722-10723-10724-10725-10726-10727-10728-10729-10730-10731-10732-10733-10734-10735-10736-10737-10738-10739-10740-10741-10742-10743-10744-10745-10746-10747-10748-10749-10750-10751-10752-10753-10754-10755-10756-10757-10758-10759-10760-10761-10762-10763-10764-10765-10766-10767-10768-10769-10770-10771-10772-10773-10774-10775-10776-10777-10778-10779-10780-10781-10782-10783-10784-10785-10786-10787-10788-10789-10790-10791-10792-10793-10794-10795-10796-10797-10798-10799-10800-10801-10802-10803-10804-10805-10806-10807-10808-10809-10810-10811-10812-10813-10814-10815-10816-10817-10818-10819-10820-10821-10822-10823-10824-10825-10826-10827-10828-10829-10830-10831-10832-10833-10834-10835-10836-10837-10838-10839-10840-10841-10842-10843-10844-10845-10846-10847-10848-10849-10850-10851-10852-10853-10854-10855-10856-10857-10858-10859-10860-10861-10862-10863-10864-10865-10866-10867-10868-10869-10870-10871-10872-10873-10874-10875-10876-10877-10878-10879-10880-10881-10882-10883-10884-10885-10886-10887-10888-10889-10890-10891-10892-10893-10894-10895-10896-10897-10898-10899-10900-10901-10902-10903-10904-10905-10906-10907-10908-10909-10910-10911-10912-10913-10914-10915-10916-10917-10918-10919-10920-10921-10922-10923-10924-10925-10926-10927-10928-10929-10930-10931-10932-10933-10934-10935-10936-10937-10938-10939-10940-10941-10942-10943-10944-10945-10946-10947-10948-10949-10950-10951-10952-10953-10954-10955-10956-10957-10958-10959-10960-10961-10962-10963-10964-10965-10966-10967-10968-10969-10970-10971-10972-10973-10974-10975-10976-10977-10978-10979-10980-10981-10982-10983-10984-10985-10986-10987-10988-10989-10990-10991-10992-10993-10994-10995-10996-10997-10998-10999-11000-11001-11002-11003-11004-11005-11006-11007-11008-11009-11010-11011-11012-11013-11014-11015-11016-11017-11018-11019-11020-11021-11022-11023-11024-11025-11026-11027-11028-11029-11030-11031-11032-11033-11034-11035-11036-11037-11038-11039-11040-11041-11042-11043-11044-11045-11046-11047-11048-11049-11050-11051-11052-11053-11054-11055-11056-11057-11058-11059-11060-11061-11062-11063-11064-11065-11066-11067-11068-11069-11070-11071-11072-11073-11074-11075-11076-11077-11078-11079-11080-11081-11082-11083-11084-11085-11086-11087-11088-11089-11090-11091-11092-11093-11094-11095-11096-11097-11098-11099-11100-11101-11102-11103-11104-11105-11106-11107-11108-11109-11110-11111-11112-11113-11114-11115-11116-11117-11118-11119-11120-11121-11122-11123-11124-11125-11126-11127-11128-11129-11130-11131-11132-11133-11134-11135-11136-11137-11138-11139-11140-11141-11142-11143-11144-11145-11146-11147-11148-11149-11150-11151-11152-11153-11154-11155-11156-11157-11158-11159-11160-11161-11162-11163-11164-11165-11166-11167-11168-11169-11170-11171-11172-11173-11174-11175-11176-11177-11178-11179-11180-11181-11182-11183-11184-11185-11186-11187-11188-11189-11190-11191-11192-11193-11194-11195-11196-11197-11198-11199-11200-11201-11202-11203-11204-11205-11206-11207-11208-11209-11210-11211-11212-11213-11214-11215-11216-11217-11218-11219-11220-11221-11222-11223-11224-11225-11226-11227-11228-11229-11230-11231-11232-11233-11234-11235-11236-11237-11238-11239-11240-11241-11242-11243-11244-11245-11246-11247-11248-11249-11250-11251-11252-11253-11254-11255-11256-11257-11258-11259-11260-11261-11262-11263-11264-11265-11266-1126

Matches 9; Conservative 1; Miscellaneous 4, including 2 maps;

7 PRRHPPSS 20

Figure 1 consists of two Western blot panels. The top panel shows p38 phosphorylation in whole cell lysates from untreated (control) and treated (LPS) cells. The bottom panel shows p38 phosphorylation in the cytosol fraction after treatment with LPS. Molecular weight markers are indicated on the left.

RESULT 10

AAV58855

ID AAY58855 standard; Peptide; 16 AA.

AC AAY58855;

08-MAY-2000 (first entry)

Membrane binding element used in anti-angiogenic poly(vinylidene fluoride) (PVDF) membranes

Anti-angiogenic; angiogenesis inhibitor; neovascularisation; cancer; tumour; therapy.

OS Synthetic.

WC200004052.A2.

27-JAN-2000.

16-JUL-1999: 99WO-GB02292

[illegible]

(ADPR-) ADPROTECH PLC

XX
PI Smith RAG. Bright CR. Steward M. Cox VE.

WPI: 2000-182406/ 6

XX
PT New soluble derivative of anti-analogous polypeptide useful for
PT treatment of primary or secondary cancers, containing covalently attached
PT membrane-binding elements for targeting -

PS Claim 12; Page 32; 36pp; English.

The present sequence is a claimed example of a lysine-rich peptide membrane binding element (MBE) that can be utilised in novel soluble derivatives (i) of anti-angiogenic polypeptides of the invention, (ii) conjugates of more heterogeneous MBEs with low membrane affinity that are covalently attached to a soluble anti-angiogenic polypeptide such as a soluble version of human plasminogen fragments of related proteins containing kringle domains, fragments of collagen or prolectin, neutralising antibodies against receptors for angiogenic mediators, and antagonists of integrins involved in angiogenesis. The MBEs interact independently with thermodynamic affinity with components of the vascular endothelium, i.e. fibroblasts, and delivery of the anti-angiogenic polypeptide to cell membranes and sites of active angiogenesis, particularly in the endothelium, and therefore increase the local concentration and hence the risk of adverse effects in tumour tissues, decrease the vasculature. They are used in a claimed method of treatment of tumour.

RESULT 14

AAE01872
ID AAE01872 standard; peptide; 15 AA.

XX
AC AAE01872;

XX
DT 31-JUL-2001 (first entry)

XX
DE Human diacylglycerol kinase (DGK) zeta partial MAPCKS domain.

XX
KW Human; catalyst; diacylglycerol; DAG; phosphatidic acid; DAG modification;
KW diacylglycerol kinase zeta; DGK; MAPCKS domain;
KW myristoylated alanine-rich C kinase substrate.

XX
OS Homo sapiens.

XX
PN US6221659-B1.

XX
PD 24-APR-2001.

XX
PF 25-AUG-1999; 99US-0382911.

XX
PR 22-APR-1996; 96US-0016210.

XX
PR 22 APR 1997; 97US-0845483.

XX
PA (UTAH) UNIV UTAH RES FOUND.

XX
PI Prescott SM, Bunting M, Tang W, Tappan M;

XX
DF WPI; 2001-327248/34.

XX
PT New DNAs of the human diacylglycerol kinase, useful for regulating the
PT levels of diacylglycerol kinase in cells to enhance the conversion of
PT diacylglycerol to phosphatidic acid, thereby increasing intracellular
PT acid levels.

XX
PS Disclosure; Column 10; 9pp; English.

XX
CC The patent discloses novel human diacylglycerol kinase (DGK) and novel
CC novel diacylglycerol kinase opsin, diacylglycerol kinase zeta,
CC diacylglycerol kinase zeta 2 and their corresponding cDNAs. Human
CC diacylglycerol kinase DNA is useful for coding human diacylglycerol
CC kinase, which is useful for catalyzing the conversion of diacylglycerol
CC to phosphatidic acid. In particular, the human diacylglycerol kinase
CC and its DNA are useful for decreasing intracellular levels of diacylglycerol
CC glycerol (DAG) and for increasing intracellular levels of phosphatidic
CC acid in cells.

XX
CC The present sequence is partial myristoylated alanine-rich C-kinase
CC substrate (MARCKS) domain of human diacylglycerol kinase (DGK) zeta
CC protein.

XX
SQ Sequence 15 AA;

Query Match 36.5%, Score 40, 18 aa, Length 16;

Best Local Similarity 80.0%; Pred No. 26;

Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 9 KVVPPSPFP 18

DB 1 KVVPPSPFP 10

RESULT 15

AAE01868
ID AAE01868 standard; peptide; 18 AA.

XX
AC AAE01868;

XX
DT 31-JUL-2001 (first entry)

XX
DE Human diacylglycerol kinase (DGK) zeta MAPCKS domain.

XX

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FW Human; catalyst; diacylglycerol; DAG; phosphatidic acid; DAG modulator;
 FW diacylglycerol kinase zeta, PDB; MAPK3 domain;
 FW myristoylated alanine rich C-kinase substrate.

XX OS Homo sapiens.

XX PN US6221658-B1.

XX PD 24 APR-2001.

XX PF 25-AUG-1999; 99US-0382911.

XX PR 22-APR-1997; 96US-0046210.

XX PR 22-APR-1997; 97US-0841483.

XX PA (UTAH) UNIV UTAH RES FOUND.

XX PI Prescott SM, Runtang M, Tang W, Topham M;

XX DP WFI; 2001 327348/34.

XX PT New DNAs of the human diacylglycerol kinase, useful for modulating the
 PT levels of diacylglycerol kinase in cells to catalyze the conversion of
 PT diacylglycerol to phosphatidic acid, therefore increasing phosphatidic
 PT acid levels.

XX PS Example 12; Column 26; 74pp; English.

XX CC The patent discloses novel human diacylglycerol kinase (DAGK) isoforms
 CC namely diacylglycerol kinase epsilon, diacylglycerol kinase zeta,
 CC diacylglycerol kinase eta and their corresponding cDNAs. Human
 CC diacylglycerol kinase cDNA is useful for coding human diacylglycerol
 CC kinase, which is useful for catalyzing the conversion of diacylglycerol
 CC to phosphatidic acid. In particular, the human diacylglycerol kinase
 CC and its DNA are useful for decreasing intracellular levels of diacyl-
 CC glycerol (DAG) and for increasing intracellular levels of phosphatidic
 CC acid in cells.

XX CC The present sequence is the myristoylated alanine-rich C-kinase
 CC substrate (MARCKS) domain of human diacylglycerol kinase (DAGK)
 CC zeta protein.

XX SO Sequence 18 AA;

Query Match 39.5%; Score 40; DB 22; Length 18;

Best Local Similarity 80.0%; Pred. No. 31;

Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 9 KKKKRSFKK 18

|||||

DB 4 KKKKRSFKK 13

Search completed: March 3, 2003, 06:56:01
 Job time : 34 secs

bioinfo version 3.1.1
 1993 - 2003 Copyright 1993

mini sw model

1. 1993/04 : Search for 10 records
 (with 1000 hits)
 60,000 hits will update/seq

11

SEQUENCE 20

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20 31 29.8 13 9 US-09-805-301-45
 21 31 29.8 13 9 US-09-805-301-102
 22 31 29.8 14 9 US-09-805-301-8
 23 31 29.8 14 9 US-09-805-301-46
 24 31 29.8 15 9 US-09-805-301-102
 25 31 29.8 15 9 US-09-805-301-102
 26 31 29.8 15 9 US-09-805-301-47
 27 31 29.8 15 9 US-09-805-301-103
 28 31 29.8 15 9 US-09-805-301-103
 29 31 29.8 16 9 US-09-805-301-103
 30 31 29.8 16 9 US-09-805-301-103
 31 31 29.8 16 9 US-09-805-301-48
 32 31 29.8 16 9 US-09-805-301-48
 33 31 29.8 16 9 US-09-805-301-104
 34 31 29.8 16 9 US-09-805-301-104
 35 31 29.8 16 9 US-09-805-301-104
 36 31 29.8 17 9 US-09-805-301-11
 37 31 29.8 17 9 US-09-805-301-49
 38 31 29.8 17 9 US-09-805-301-105
 39 31 29.8 18 9 US-09-805-301-12
 40 31 29.8 18 9 US-09-805-301-50
 41 31 29.8 18 9 US-09-805-301-106
 42 31 29.8 19 9 US-09-805-301-13
 43 31 29.8 19 9 US-09-805-301-51
 44 31 29.8 19 9 US-09-805-301-107
 45 31 29.8 20 9 US-09-805-301-114

ALIGNMENTS

RESULT 1

US-09-804-681-8
 : Sequence 8, Affiliation US/2004691
 : Patent No. US2002006154A1
 : GENERAL INFORMATION:
 : APPLICANT: Tsuboi, Robert Y.
 : TITLE OF INVENTION: Assays for Protein Kinases Using
 : Fluorescent Histone Substrates
 : NUMBER OF SEQUENCES: 48
 : REFERENCE SEQUENCE: 48
 : ADDRESS: Townsend and Townsend and Crew LLP
 : STREET: Two Embarcadero Center, Eighth Floor
 : CITY: San Francisco
 : STATE: California
 : COUNTRY: USA
 : ZIP: 94111-3834
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : OPERATING SYSTEM: PC-PC/MS DOS
 : SOFTWARE: Pat. In. Release #100, Version #1.0

CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/2004691
 : FILING DATE: 19-Jun-2001
 : CLASSIFICATION: Unknown
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: 08/573,865
 : FILING DATE: Unknown
 : ATTORNEY/AGENT INFORMATION:
 : NAME: Storella, John S.
 : REGISTRATION NUMBER: 32,944
 : TELEPHONE: 415-574-2000
 : TELEFAX: 415-574-0300
 : INFORMATION FOR SEQ ID NO: 8:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 9 amino acids
 : TYPE: amino acid
 : STRANDEDNESS: Unknown
 : TOPOLOGY: Linear

US-09-804-681-8
 : Sequence 8, Appl
 : Sequence 12, Appl
 : Sequence 26, Appl
 : Sequence 42, Appl
 : Sequence 1959, Ap
 : Sequence 1960, Ap
 : Sequence 32, Appl
 : Sequence 30, Appl
 : Sequence 51, Appl
 : Sequence 97, Appl
 : Sequence 196, Appl
 : Sequence 1, Appl
 : Sequence 31, Appl
 : Sequence 28, Appl
 : Sequence 4, Appl
 : Sequence 34, Appl
 : Sequence 110, App
 : Sequence 1, Appl
 : Sequence 27, Appl

SUMMARY

of results predicted by change to have a
 equal to the score of the result being printed,
 of the total score distribution.

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1 MOLECULE TYPE: peptide
2 SEQUENCE DESCRIPTION: SEQ ID NO: 3
US-09-884-681-8

Query Match: 4423 Score 46 DE 10 Length 10
Pos 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20
Matches 9: Conservative 0: Mismatches 0: Indels 0: Gaps 0

CY 8 KKKKKKKKK 17
DE 1 KKKKKKKKK 9

RESULT 2
US-09-124-280A-12
1 Query Match: 4423 Score 46 DE 10 Length 10
2 Best Local Similarity: 90.0% Ident: 10.0%
3 Patent No. US2002034520A1
4 GENERAL INFORMATION:
5 APPLICANT: FORTO, Massimo
6 TITLE OF INVENTION: VACCINES FOR PREVENTION OF GRAM-
7 TITLE OF INVENTION: REMANENT BACTERIAL INFECTIONS AND
8 NUMBER OF SEQUENCES: 45
9 CORRESPONDENCE ADDRESS:
10 ADDRESSEE: Hedman, Gibson & Costigan
11 STREET: 1185 Avenue of the Americas
12 CITY: New York
13 STATE: New York
14 COUNTRY: USA
15 ZIP: 10036
16 COMPUTER READABLE FORM:
17 MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
18 COMPUTER: IBM PS/2
19 OPERATING SYSTEM: DOS
20 SOFTWARE: Word Perfect 5.1
21 CURRENT APPLICATION DATA:
22 APPLICATION NUMBER: US/09/124-280A
23 FILING DATE: July 20, 1998
24 CLASSIFICATION: 424
25 PRIOR APPLICATION DATA:
26 APPLICATION NUMBER:
27 FILING DATE:
28 ATTORNEY/AGENT INFORMATION:
29 NAME: Costigan, James V.
30 REGISTRATION NUMBER: 25,669
31 REFERENCE/DOCKET NUMBER: 574 009
32 TELECOMMUNICATION INFORMATION:
33 TELEPHONE: (212) 302-8989
34 TELEFAX: (212) 302-8989
35 INFORMATION FOR SEQ ID NO: 12:
36 SEQUENCE CHARACTERISTICS:
37 LENGTH: 10 amino acids
38 TYPE: amino acid
39 TOPOLOGY: circular
40 US-09-124-280A-12

Query Match: 4423 Score 46 DE 10 Length 10
2 Best Local Similarity: 90.0% Ident: 10.0%
3 Patent No. US2002034520A1
4 GENERAL INFORMATION:
5 APPLICANT: FORTO, Massimo
6 TITLE OF INVENTION: VACCINES FOR PREVENTION OF GRAM-
7 TITLE OF INVENTION: REMANENT BACTERIAL INFECTIONS AND
8 NUMBER OF SEQUENCES: 45
9 CORRESPONDENCE ADDRESS:
10 ADDRESSEE: Hedman, Gibson & Costigan
11 STREET: 1185 Avenue of the Americas
12 CITY: New York
13 STATE: New York
14 COUNTRY: USA
15 ZIP: 10036
16 COMPUTER READABLE FORM:
17 MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
18 COMPUTER: IBM PS/2
19 OPERATING SYSTEM: DOS
20 SOFTWARE: Word Perfect 5.1
21 CURRENT APPLICATION DATA:
22 APPLICATION NUMBER: US/09/124-280A
23 FILING DATE: July 20, 1998
24 CLASSIFICATION: 424
25 PRIOR APPLICATION DATA:
26 APPLICATION NUMBER:
27 FILING DATE:
28 ATTORNEY/AGENT INFORMATION:
29 NAME: Costigan, James V.
30 REGISTRATION NUMBER: 25,669
31 REFERENCE/DOCKET NUMBER: 574 009
32 TELECOMMUNICATION INFORMATION:
33 TELEPHONE: (212) 302-8989
34 TELEFAX: (212) 302-8989
35 INFORMATION FOR SEQ ID NO: 12:
36 SEQUENCE CHARACTERISTICS:
37 LENGTH: 10 amino acids
38 TYPE: amino acid
39 TOPOLOGY: circular
40 US-09-124-280A-12

CY 8 KKKKKKKKK 17
DE 1 KKKKKKKKK 9

RESULT 3
US-09-124-280A-12
1 Query Match: 4423 Score 46 DE 10 Length 10
2 Best Local Similarity: 90.0% Ident: 10.0%
3 Patent No. US2002034520A1
4 GENERAL INFORMATION:
5 APPLICANT: FORTO, Massimo
6 TITLE OF INVENTION: VACCINES FOR PREVENTION OF GRAM-
7 TITLE OF INVENTION: REMANENT BACTERIAL INFECTIONS AND
8 NUMBER OF SEQUENCES: 45
9 CORRESPONDENCE ADDRESS:
10 ADDRESSEE: Hedman, Gibson & Costigan
11 STREET: 1185 Avenue of the Americas
12 CITY: New York
13 STATE: New York
14 COUNTRY: USA
15 ZIP: 10036
16 COMPUTER READABLE FORM:
17 MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
18 COMPUTER: IBM PS/2
19 OPERATING SYSTEM: DOS
20 SOFTWARE: Word Perfect 5.1
21 CURRENT APPLICATION DATA:
22 APPLICATION NUMBER: US/09/124-280A
23 FILING DATE: July 20, 1998
24 CLASSIFICATION: 424
25 PRIOR APPLICATION DATA:
26 APPLICATION NUMBER:
27 FILING DATE:
28 ATTORNEY/AGENT INFORMATION:
29 NAME: Costigan, James V.
30 REGISTRATION NUMBER: 25,669
31 REFERENCE/DOCKET NUMBER: 574 009
32 TELECOMMUNICATION INFORMATION:
33 TELEPHONE: (212) 302-8989
34 TELEFAX: (212) 302-8989
35 INFORMATION FOR SEQ ID NO: 12:
36 SEQUENCE CHARACTERISTICS:
37 LENGTH: 10 amino acids
38 TYPE: amino acid
39 TOPOLOGY: circular
40 US-09-124-280A-12

CY 8 KKKKKKKKK 17
DE 1 KKKKKKKKK 9
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1 FILE REFERENCE: 012960
2 CURRENT APPLICATION NUMBER: US/09/124-280A
3 CURRENT FILING DATE: 2001-10-24
4 PRIOR APPLICATION NUMBER: US/09/101,751
5 PRIOR FILING DATE: 1999-01-29
6 PRIOR APPLICATION NUMBER: US/09/101,751
7 PRIOR FILING DATE: 1999-01-29
8 PRIOR APPLICATION NUMBER: US/08/700,846
9 PRIOR FILING DATE: 1998-09-21
10 PRIOR APPLICATION NUMBER: US/08/701,124
11 PRIOR FILING DATE: 1998-09-21
12 PRIOR APPLICATION NUMBER: US/08/563,366
13 PRIOR FILING DATE: 1998-11-28
14 NUMBER OF SEQ ID NOS: 94
15 SOFTWARE: PatentIn Ver. 2.1
16 SEQ ID NO: 16
17 LENGTH: 19
18 TYPE: PRT
19 ORGANISM: Artificial Sequence
20 FEATURE:
21 OTHER INFORMATION: Synthetic
22 US-09-124-280A-12
23 Query Match: 3783 Score 39 DE 9 Length 19
24 Best Local Similarity: 93.8% Ident: 10.0%
25 Matches 2: Conservative 4: Mismatches 4: Indels 0: Gaps 0

CY 4 NETHKPKPKPKPK 19
DE 1 NETHKPKPKPKPK 16

RESULT 4
US-09-124-280A-42
1 Query Match: 4423 Score 46 DE 10 Length 10
2 Best Local Similarity: 90.0% Ident: 10.0%
3 Patent No. US2002034520A1
4 GENERAL INFORMATION:
5 APPLICANT: FORTO, Massimo
6 TITLE OF INVENTION: VACCINES FOR PREVENTION OF GRAM-
7 TITLE OF INVENTION: REMANENT BACTERIAL INFECTIONS AND
8 NUMBER OF SEQUENCES: 45
9 CORRESPONDENCE ADDRESS:
10 ADDRESSEE: Hedman, Gibson & Costigan
11 STREET: 1185 Avenue of the Americas
12 CITY: New York
13 STATE: New York
14 COUNTRY: USA
15 ZIP: 10036
16 COMPUTER READABLE FORM:
17 MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
18 COMPUTER: IBM PS/2
19 OPERATING SYSTEM: DOS
20 SOFTWARE: Word Perfect 5.1
21 CURRENT APPLICATION DATA:
22 APPLICATION NUMBER: US/09/124-280A
23 FILING DATE: July 20, 1998
24 CLASSIFICATION: 424
25 PRIOR APPLICATION DATA:
26 APPLICATION NUMBER:
27 FILING DATE:
28 ATTORNEY/AGENT INFORMATION:
29 NAME: Costigan, James V.
30 REGISTRATION NUMBER: 25,669
31 REFERENCE/DOCKET NUMBER: 574 009
32 TELECOMMUNICATION INFORMATION:
33 TELEPHONE: (212) 302-8989
34 TELEFAX: (212) 302-8989
35 INFORMATION FOR SEQ ID NO: 42:
36 SEQUENCE CHARACTERISTICS:
37 LENGTH: 10 amino acids
38 TYPE: amino acid
39 TOPOLOGY: circular
40 US-09-124-280A-42
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Query Match 35.6% Score 37; DB 1; Length 10;
Best Local Similarity 52.8%; Pred. No. 49;
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 SPSNETPKYKX 13
DB 2 SPVMSPKYKXQ 14

US-09-999-724-38

Sequence 38, Application US/09999724
Publication No. US2001002355A1
GENERAL INFORMATION:
APPLICANT: WICKHAM, THOMAS J.
APPLICANT: KOVEDI, IMRE
TITLE OF INVENTION: VECTORS AND METHODS FOR GENE TRANSFER
FILE REFERENCE: 212960
CURRENT APPLICATION NUMBER: US/09/999,724
CURRENT FILING DATE: 2001-10-24
PRIOR APPLICATION NUMBER: US 08/701,751
PRIOR FILING DATE: 1999-01-29
PRIOR APPLICATION NUMBER: WO 98US19158
PRIOR FILING DATE: 1996-11-27
PRIOR APPLICATION NUMBER: US 08/701,751
PRIOR FILING DATE: 1996-08-21
PRIOR APPLICATION NUMBER: US 08/701,751
PRIOR FILING DATE: 1996-08-21
PRIOR APPLICATION NUMBER: US 08/563,368
PRIOR FILING DATE: 1995-11-28
NUMBER OF SEQ ID NOS: 94
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 38
LENGTH: 15
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic
US-09-999-724-38

Query Match 33.7% Score 35; DB 9; Length 15;
Best Local Similarity 60.0%; Pred. No. 49;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

US-09-954-866-30

Sequence 30, Application US/09866486
Patent No. US2002012656A1
GENERAL INFORMATION:
APPLICANT: Lloyd, R. Stephen
APPLICANT: McCulloch, Amanda K.
APPLICANT: Nguyen, Khoa
TITLE OF INVENTION: DNA REPAIR POLYMERASES AND METHODS OF USE
FILE REFERENCE: 265,00170101
CURRENT APPLICATION NUMBER: US/03/864,866
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/246,279
PRIOR FILING DATE: 2000-05-23
NUMBER OF SEQ ID NOS: 49
SOFTWARE: PatentIn version 3.0
SEQ ID NO 30
LENGTH: 8
TYPE: PRT

TYPE: PRT
ORGANISM: Homo sapiens
US-09-902-941-1960

Query Match 35.6% Score 37; DB 1; Length 10;
Best Local Similarity 52.8%; Pred. No. 49;
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 SPSNETPKYKX 13
DB 2 SPVMSPKYKXQ 14

RESULT 7

US-09-999-724-38
Sequence 38, Application US/09999724
Publication No. US2001002355A1
GENERAL INFORMATION:
APPLICANT: WICKHAM, THOMAS J.
APPLICANT: KOVEDI, IMRE
TITLE OF INVENTION: VECTORS AND METHODS FOR GENE TRANSFER
FILE REFERENCE: 212960
CURRENT APPLICATION NUMBER: US/09/999,724
CURRENT FILING DATE: 2001-10-24
PRIOR APPLICATION NUMBER: US 08/701,751
PRIOR FILING DATE: 1999-01-29
PRIOR APPLICATION NUMBER: WO 98US19158
PRIOR FILING DATE: 1996-11-27
PRIOR APPLICATION NUMBER: US 08/701,751
PRIOR FILING DATE: 1996-08-21
PRIOR APPLICATION NUMBER: US 08/701,751
PRIOR FILING DATE: 1996-08-21
PRIOR APPLICATION NUMBER: US 08/563,368
PRIOR FILING DATE: 1995-11-28
NUMBER OF SEQ ID NOS: 94
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 38
LENGTH: 15
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic
US-09-999-724-38

Query Match 33.7% Score 35; DB 9; Length 15;
Best Local Similarity 60.0%; Pred. No. 49;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 4 NETPKYKX 13
DB 1 NDTPKYKX 10

RESULT 8

US-09-954-866-30
Sequence 30, Application US/09866486
Patent No. US2002012656A1
GENERAL INFORMATION:
APPLICANT: Lloyd, R. Stephen
APPLICANT: McCulloch, Amanda K.
APPLICANT: Nguyen, Khoa
TITLE OF INVENTION: DNA REPAIR POLYMERASES AND METHODS OF USE
FILE REFERENCE: 265,00170101
CURRENT APPLICATION NUMBER: US/03/864,866
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/246,279
PRIOR FILING DATE: 2000-05-23
NUMBER OF SEQ ID NOS: 49
SOFTWARE: PatentIn version 3.0
SEQ ID NO 30
LENGTH: 8
TYPE: PRT

ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: A consensus nucleic acid localization sequence
US-09-864-866 30

Query Match 32.7% Score 34; DB 10; Length 8;
Best Local Similarity 85.7% Pred No. 1.5e+05;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0

QY 7 PKKKKK 13
DB 1 PKKKKK 7

RESULT 9
US-09-910-386A-53
Sequence 53, Application US/2001/0386A
Patent No. US200200401A1
GENERAL INFORMATION:
APPLICANT: Rohan, Pamela C.
APPLICANT: Wang, Guo Zhang
APPLICANT: Song, Wen Yang
APPLICANT: Hulbert, Scott
APPLICANT: Richner, Todd
TITLE OF INVENTION: Peptides and Materials for Conferring
Disease Resistance in Plants
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-505/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/910.386A
FILING DATE: 13 AUG 1997
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 117, 118, 120, 121, 122, 123
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-8400
TELEFAX: (415) 576-8400

INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Modified site
LOCATION: 13
OTHER INFORMATION: Product "OTHER"
OTHER INFORMATION: Roles "Mod - 110, Mod, Thr, Asn, Lys,
OTHER INFORMATION: Ser at 63"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 14
OTHER INFORMATION: Product "OTHER"
OTHER INFORMATION: Roles "Mod - 110, Mod, Thr, Asn, Lys,
OTHER INFORMATION: Ser at 63"
US-09-910-386A-53

Query Match 32.7% Score 34; DB 9; Length 14;
Best Local Similarity 85.7% Pred No. 1.5e+05;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0

QY 7 PKKKKK 13
DB 2 PKKKKK 8

RESULT 10
US-09-945-349-87
Sequence 87, Application US/2001/0945249
Patent No. US20020168748A1
GENERAL INFORMATION:
APPLICANT: BERLIN, VIVIAN
APPLICANT: SAMAGNEZ, VERONIQUE
APPLICANT: SMITH, SUSAN E.
TITLE OF INVENTION: ASSAYS AND FRAGMENTS FOR IDENTIFYING ANTI-EPIDEM AGENTS,
TITLE OF INVENTION: AND USES RELATED THERETO
FILE REFERENCE: WIV 074 07
CURRENT APPLICATION NUMBER: US/09/0945249
CURRENT FILING DATE: 2001-08-11
PRIOR APPLICATION NUMBER: 09/041,990
PRIOR FILING DATE: 2001-01-13
PRIOR APPLICATION NUMBER: 09/771,212
PRIOR FILING DATE: 1996-12-20
PRIOR APPLICATION NUMBER: 09/711,119
PRIOR FILING DATE: 1996-04-11
NUMBER OF SEQ ID NOS: 89
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO: 87

LENGTH: 15
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Peptide that
OTHER INFORMATION: corresponds to the C-terminal of PASE OF GUTASE
OTHER INFORMATION: substrates
US-09-945-349-87

Query Match 32.7% Score 34; DB 9; Length 15;
Best Local Similarity 77.8% Pred No. 85;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0

QY 4 NETPKKKKK 12
DB 3 NETPKKKKK 11

RESULT 11
US-09-071-838-196
Sequence 19, Application US/2001/071838
Patent No. US200201501A1
GENERAL INFORMATION:
APPLICANT: Fischer, Robert L.
APPLICANT: Chad, Nir
APPLICANT: Miyase, Tomohiro
APPLICANT: Vadevati, Pamin
APPLICANT: Maragostian, Linda
APPLICANT: Harada, John
APPLICANT: Goldberg, Robert B.
TITLE OF INVENTION: Nucleic Acids That Control Seed and
TITLE OF INVENTION: Plant Development in Plants
NUMBER OF SEQUENCES: 324
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-505/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30

APPLICANT: Zhu, Quan
APPLICANT: Laurent Olivier
APPLICANT: Marasco Wayne A.
APPLICANT: Scherman, Daniel
TITLE OF INVENTION: DELIVERY
FILE REFERENCE: 23611-A USA
CURRENT APPLICATION NUMBER: US/09/888,721
PRIOR FILING DATE: 2001-06-25
PRIOR APPLICATION NUMBER: 60/213,653
NUMBER OF SEQ ID NOS: 45
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 31
LENGTH: 14
TYPE: PRT
ORGANISM: Homo sapiens
US-09-888-721-31

Query Match 31.78; Score 33; DB 17; Length 14;
Best Local Similarity 60.09; Pred. No. 1,114,02;
Matches 6; Conservative 2; Mismatches 2; Gaps 0;

QY 3 SNETPKYKX 12
DB 4 APTPKYKX 13

RESULT 14
US-09-736-959A-28

Sequence 28, Application US/0916050A
Patent No. US20020076415A1
GENERAL INFORMATION:
APPLICANT: University of Southern California
APPLICANT: OU, Jing-Hsiung
APPLICANT: XU, Zhenming
TITLE OF INVENTION: HEPATITIS C VIRUS GENE PRODUCT TS
FILE REFERENCE: 13761-742
CURRENT APPLICATION NUMBER: US/09/34,939A
CURRENT FILING DATE: 2000-12-14
PRIOR APPLICATION NUMBER: US 60/170,835
PRIOR FILING DATE: 1999-12-14
NUMBER OF SEQ ID NOS: 32
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 28
LENGTH: 16
TYPE: PRT
ORGANISM: Hepatitis C Virus (HCV); subtype
US-09-736-959A-28

Query Match 31.78; Score 33; DB 10; Length 16;
Best Local Similarity 54.58; Pred. No. 1,224,02;
Matches 6; Conservative 2; Mismatches 3; Gaps 0;

QY 3 SNETPKYKX 13
DB 3 TNPXPKYKX 13

RESULT 15
US-09-950-692-4

Sequence 4, Application US/9950692
Patent No. US6000106701A1
GENERAL INFORMATION:
APPLICANT: Goulet, Said A
TITLE OF INVENTION: Quantitation of individual Protein Phosphorylation
FILE REFERENCE: Kinase
CURRENT APPLICATION NUMBER: US/09/950,692
CURRENT FILING DATE: 2001-06-27
PRIOR APPLICATION NUMBER: 08/208,573
PRIOR FILING DATE: 1994-03-04
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn Ver. 2.0

APPLICANT: Zhu, Quan
APPLICANT: Laurent Olivier
APPLICANT: Marasco Wayne A.
APPLICANT: Scherman, Daniel
TITLE OF INVENTION: DELIVERY
FILE REFERENCE: 23611-A USA
CURRENT APPLICATION NUMBER: US/09/888,721
PRIOR FILING DATE: 2001-06-25
PRIOR APPLICATION NUMBER: 60/213,653
NUMBER OF SEQ ID NOS: 45
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 31
LENGTH: 14
TYPE: PRT
ORGANISM: Homo sapiens
US-09-888-721-31

Query Match 31.78; Score 33; DB 17; Length 14;
Best Local Similarity 60.09; Pred. No. 1,114,02;
Matches 6; Conservative 2; Mismatches 2; Gaps 0;

QY 3 SNETPKYKX 12
DB 4 APTPKYKX 13

RESULT 14

US-09-736-959A-28
Sequence 28, Application US/0916050A
Patent No. US20020076415A1
GENERAL INFORMATION:
APPLICANT: University of Southern California
APPLICANT: OU, Jing-Hsiung
APPLICANT: XU, Zhenming
TITLE OF INVENTION: HEPATITIS C VIRUS GENE PRODUCT TS
FILE REFERENCE: 13761-742
CURRENT APPLICATION NUMBER: US/09/34,939A
CURRENT FILING DATE: 2000-12-14
PRIOR APPLICATION NUMBER: US 60/170,835
PRIOR FILING DATE: 1999-12-14
NUMBER OF SEQ ID NOS: 32
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 28
LENGTH: 16
TYPE: PRT
ORGANISM: Hepatitis C Virus (HCV); subtype
US-09-736-959A-28

Query Match 31.78; Score 33; DB 10; Length 16;
Best Local Similarity 54.58; Pred. No. 1,224,02;
Matches 6; Conservative 2; Mismatches 3; Gaps 0;

QY 3 SNETPKYKX 13
DB 3 TNPXPKYKX 13

RESULT 15

US-09-950-692-4
Sequence 4, Application US/9950692
Patent No. US6000106701A1
GENERAL INFORMATION:
APPLICANT: Goulet, Said A
TITLE OF INVENTION: Quantitation of individual Protein Phosphorylation
FILE REFERENCE: Kinase
CURRENT APPLICATION NUMBER: US/09/950,692
CURRENT FILING DATE: 2001-06-27
PRIOR APPLICATION NUMBER: 08/208,573
PRIOR FILING DATE: 1994-03-04
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn Ver. 2.0

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; SEQ ID NO 4
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: polypeptide
US-09-950-692-4
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Query Match 30.8% Score 32; DB 10; Length 10;
Best Local Similarity 75.0%; Pos. No. 1;1e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
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OR 2 KTPKPKKK 9
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Search completed: March 3, 2003, 07:02:11
Job time : 13 secs
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Med. Mar version 5.1.1
1991 - 2003 Copyright

using sw model

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28 35 33.7 20 2 US-08-995-173-23
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30 35 33.7 20 2 US-08-995-173-23
31 35 33.7 20 2 US-08-995-173-23
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44 35 33.7 20 2 US-08-995-173-23
45 35 33.7 20 2 US-08-995-173-23

ALIGNMENTS

RESULT 1
US-08-679-865-8
; Sequence 6, Application US/08679865
; Patent No. 5912137
; GENERAL INFORMATION:
; APPLICANT: Tsiang, Roger Y.
; APPLICANT: Cubitt, Andrew B.
; TITLE OF INVENTION: Assays for Protein Kinase Using
; TITLE OF INVENTION: Fluorescent Protein Substrates
; NUMBER OF SEQUENCES: 48
; REFERENCE ADDRESS:
; ADDRESS: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3814
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: 08/012,679, AKA
; FILING DATE: 16-JUL-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Starella, John S.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 08/012-567000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-679-865-8

Query Match 44.2%; Score 46; DP 2; Length 3;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 9; Conservative 0; Mismatches 0; Gaps 0

Cy 9 KKKKPPSPK 17

Db 1 KKKKPPSPK 9

CDR ID	Description
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2	Sequence 2, Appl
3	Sequence 3, Appl
4	Sequence 4, Appl
5	Sequence 5, Appl
6	Sequence 6, Appl
7	Sequence 7, Appl
8	Sequence 8, Appl
9	Sequence 9, Appl
10	Sequence 10, Appl
11	Sequence 11, Appl
12	Sequence 12, Appl
13	Sequence 13, Appl
14	Sequence 14, Appl
15	Sequence 15, Appl
16	Sequence 16, Appl
17	Sequence 17, Appl
18	Sequence 18, Appl
19	Sequence 19, Appl
20	Sequence 20, Appl
21	Sequence 21, Appl
22	Sequence 22, Appl
23	Sequence 23, Appl
24	Sequence 24, Appl
25	Sequence 25, Appl
26	Sequence 26, Appl
27	Sequence 27, Appl
28	Sequence 28, Appl
29	Sequence 29, Appl
30	Sequence 30, Appl
31	Sequence 31, Appl
32	Sequence 32, Appl
33	Sequence 33, Appl
34	Sequence 34, Appl
35	Sequence 35, Appl
36	Sequence 36, Appl
37	Sequence 37, Appl
38	Sequence 38, Appl
39	Sequence 39, Appl
40	Sequence 40, Appl
41	Sequence 41, Appl
42	Sequence 42, Appl
43	Sequence 43, Appl
44	Sequence 44, Appl
45	Sequence 45, Appl
46	Sequence 46, Appl
47	Sequence 47, Appl
48	Sequence 48, Appl

SUMMARY

Set of results previously shown to have a
equal to the score of the best being printed,
of the total score distribution.

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RESULT 2
US-09-263-975-H
? Sequence 2, Application US/09080376
? Patent No. 5925559
? GENERAL INFORMATION:
? APPLICANT: Tsieng, Roger Y.
? APPLICANT: Chablit, Andrew B.
? TITLE OF INVENTION: Assays for Protein Kinases Using
? TITLE OF INVENTION: Fluorescent Protein Substrates
? NUMBER OF SEQUENCES: 43
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Townsend and Townsend and Clark LLP
? STREET: Two Palomar Blvd., Suite 111
? CITY: San Francisco
? STATE: California
? COUNTRY: USA
? ZIP: 94111-3834
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC/MS-DOS
? SOFTWARE: Patent in Release #1 0, Version #1.30
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/95/221,575
? FILING DATE: 16 JUL 1995
? CLASSIFICATION: 43C
? ATTORNEY/AGENT INFORMATION:
? NAME: Storella, John S.
? REGISTRATION NUMBER: 32,944
? REFERENCE/AGENT NUMBER: 03072 060000
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (415) 576-0200
? TELEFAX: (415) 576-0300
? INFORMATION FOR SEQ ID NO: 1:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 9 amino acids
? TYPE: amino acid
? STRANDEDNESS:
? TOPOLOGY: linear
? Molecule type: peptide
US-09-699-876-H

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Copy Match 44.3%, Score 46, DB 1, Length 9
Best local similarity 100.0%, Prod No. 1.9e+05
Matches 3, Conservative 0, Mismatches 0, Indels 0,

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CY 9 KVVVFFSPY 17
| | | | |
DB 1 KVVVFFSPY 9

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RESULT 3
US-09-263-975-H
? Sequence 2, Application US/09080376
? Patent No. 5925559
? GENERAL INFORMATION:
? APPLICANT: Tsieng, Roger Y.
? APPLICANT: Chablit, Andrew B.
? TITLE OF INVENTION: Assays for Protein Kinases Using
? TITLE OF INVENTION: Fluorescent Protein Substrates
? NUMBER OF SEQUENCES: 43
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Townsend and Townsend and Clark LLP
? STREET: Two Palomar Blvd., Suite 111
? CITY: San Francisco
? STATE: California
? COUNTRY: USA
? ZIP: 94111-3834
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC/MS-DOS

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? SOFTWARE: Patent in Release #1.0, Version #1.30
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/95/221,575
? FILING DATE:
? CLASSIFICATION:
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 08/679,865
? FILING DATE: 16-JUL-1996
? ATTORNEY/AGENT INFORMATION:
? NAME: Storella, John S.
? REGISTRATION NUMBER: 32,944
? REFERENCE/AGENT NUMBER: 03072 060000
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (415) 576-0200
? TELEFAX: (415) 576-0300
? INFORMATION FOR SEQ ID NO: 8:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 9 amino acids
? TYPE: amino acid
? STRANDEDNESS:
? TOPOLOGY: linear
? Molecule type: peptide
US-09-214-913-39

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Copy Match 44.3%, Score 46, DB 4, Length 9
Best local similarity 100.0%, Prod No. 1.9e+05
Matches 3, Conservative 0, Mismatches 0, Indels 0,

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CY 9 KVVVFFSPY 17
| | | | |
DB 1 KVVVFFSPY 9

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RESULT 4
US-09-263-975-H
? Sequence 2, Application US/09080376
? Patent No. 5925559
? GENERAL INFORMATION:
? APPLICANT: Tsieng, Roger Y.
? APPLICANT: Chablit, Andrew B.
? TITLE OF INVENTION: Assays for Protein Kinases Using
? TITLE OF INVENTION: Fluorescent Protein Substrates
? NUMBER OF SEQUENCES: 43
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Townsend and Townsend and Clark LLP
? STREET: Two Palomar Blvd., Suite 111
? CITY: San Francisco
? STATE: California
? COUNTRY: USA
? ZIP: 94111-3834
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC/MS-DOS
? OPERATING SYSTEM: DOS
? SOFTWARE: Word Perfect 5.1
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/95/221,575
? FILING DATE:
? CLASSIFICATION: 514
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER:
? FILING DATE:
? ATTORNEY/AGENT INFORMATION:
? NAME: Storella, John S.
? REGISTRATION NUMBER: 32,944
? REFERENCE/AGENT NUMBER: 03072 060000
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (415) 576-0200
? TELEFAX: (415) 576-0300
? INFORMATION FOR SEQ ID NO: 12:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 10 amino acids
? TYPE: amino acid
? STRANDEDNESS: linear

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COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC DOS/MS DOS
 SOFTWARE: FASTA 3.0, Release #1.0, Version #1.0
 CURRENT APPLICATION DATA
 APPLICATION NUMBER: 09/09/1995, 177A
 FILING DATE: 16-MAR-1995
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Jackson Esq., David A.
 REGISTRATION NUMBER: 26,742
 REFERENCE/EXCISE NUMBER: 641,111A
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 201 497 1900
 TELEFAX: 201 343-1684
 TELEX: 133521
 INFORMATION FOR SEQ ID NOS: 12:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 18 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 HYPOTHETICAL: NO
 FRAGMENT TYPE: internal
 US-09-405-175A-12

Query Match 38.5%; Score 40; DB 2; Length 18;
 Best Local Similarity 38.5%; Pred No. 14;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 12 KKPSPKKS 19
 |||||
 Db 1 KKPSPKKS 8

RESULT 9
 US-08-841-483-15
 Sequence 15, Application US/0841483P
 GENERAL INFORMATION:
 APPLICANT: Prescott, Steven M.
 APPLICANT: Bunting, Michaeline
 APPLICANT: Tang, Wen
 APPLICANT: Topham, Matthew
 TITLE OF INVENTION: Methods of Use Thereof
 FILE REFERENCE: 03/01/1995
 CURRENT APPLICATION NUMBER: 08/041,192
 EARLIER FILING DATE: 1997-04-22
 EARLIER APPLICATION NUMBER: 08/041,192
 NUMBER OF SEQ ID NOS: 33
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO: 15
 LENGTH: 18
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Peptide-synthetic
 OTHER INFORMATION: peptide
 US-08-841-483-15

Query Match 38.5%; Score 40; DB 2; Length 18;
 Best Local Similarity 38.5%; Pred No. 14;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 9 KKPSPKKS 12
 |||||
 Db 4 KKPSPKKS 13

RESULT 10
 US-09-382-911-15
 Sequence 16, Application US/09382911
 FILE NO: 001758
 GENERAL INFORMATION:
 APPLICANT: Prescott, Steven M.
 APPLICANT: Bunting, Michaeline
 APPLICANT: Tang, Wen
 APPLICANT: Topham, Matthew
 TITLE OF INVENTION: Methods of Use Thereof
 FILE REFERENCE: 03/01/1995
 CURRENT APPLICATION NUMBER: 09/093,911
 EARLIER FILING DATE: 1997-04-22
 EARLIER APPLICATION NUMBER: 08/041,192
 PRIOR FILING DATE: 1997-04-22
 PRIOR APPLICATION NUMBER: 08/041,192
 NUMBER OF SEQ ID NOS: 33
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO: 15
 LENGTH: 18
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Peptide-synthetic
 OTHER INFORMATION: peptide
 US-09-382-911-15

Query Match 38.5%; Score 40; DB 4; Length 18;
 Best Local Similarity 38.5%; Pred No. 9.8;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 9 KKPSPKKS 18
 |||||
 Db 4 KKPSPKKS 13

RESULT 11
 US-09-101-751A-36
 Sequence 36, Application US/09101751A
 FILE NO: 045253
 GENERAL INFORMATION:
 APPLICANT: WICKHAM, THOMAS J.
 APPLICANT: KOVEDI, IMRE
 APPLICANT: BRUSH, PHILIPAS E.
 TITLE OF INVENTION: METHODS AND MEANS FOR THE TREATMENT OF CELLS
 FILE REFERENCE: 05710
 CURRENT APPLICATION NUMBER: 09/101,751A
 EARLIER FILING DATE: 1998-01-09
 EARLIER APPLICATION NUMBER: 08/053,117
 PRIOR FILING DATE: 1996-11-27
 PRIOR APPLICATION NUMBER: 08/053,117
 PRIOR FILING DATE: 1996-08-21
 PRIOR APPLICATION NUMBER: 08/053,117
 PRIOR FILING DATE: 1996-08-21
 PRIOR APPLICATION NUMBER: 08/053,117
 PRIOR FILING DATE: 1995-11-28
 NUMBER OF SEQ ID NOS: 94
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO: 36
 LENGTH: 19
 TYPE: PRT
 ORGANISM: Unknown Organism
 FEATURE:
 NAME/REV: misc feature
 LOCATION: (1..17)
 OTHER INFORMATION: Description of Unknown Organism: Artificial
 OTHER INFORMATION: Sequence
 US-09-101-751A-36

Query Match 37.5%; Score 39; DB 4; Length 19;
 Best Local Similarity 50.0%; Pred. No. 14;

||||:|||||
 3 PPFEMKPEVNE 15

RESULT 15

US-08-456-112B-42
 : Sequence 42, Application US/08456112P
 : Patent No. 5834430
 : GENERAL INFORMATION:
 : APPLICANT: Porro, Massimo
 : TITLE OF INVENTION: POTENTIATION OF ANTIBIOTICS
 : NUMBER OF SEQUENCES: 45
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: Hedman, Gibson & Costigan
 : STREET: 1185 Avenue of the Americas
 : CITY: New York
 : STATE: New York
 : COUNTRY: USA
 : ZIP: 10036
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Disette, 3.50 inch, 1.44 Mb storage
 : COMPUTER: IFAHNG FICP 486
 : OPERATING SYSTEM: DOS
 : SOFTWARE: Word Perfect 5.1
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/08/456-112B
 : FILING DATE: May 31, 1995
 : CLASSIFICATION: 514
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER:
 : FILING DATE:
 : ATTORNEY/AGENT INFORMATION:
 : NAME: Costigan, James V.
 : REGISTRATION NUMBER: 25,669
 : REFERENCE/DOCKET NUMBER: 576-004
 : TELECOMMUNICATION INFORMATION:
 : TELEPHONE: (212) 302-8989
 : TELEFAX: (212) 302-8998
 : INFORMATION FOR SEQ ID NO. 42:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 10 amino acids
 : TYPE: amino acid
 : TOPOLOGY: circular
 : US-08-456-112B-42

Query Match 35.63; Score 37; DB 2; Length 10;
 Biological Similarity 70.93; Ref. No. 15;
 Matches 7; Complement 1; Mismatches 1; Indels 0; Gaps 0;

QY 9 PPFEMKPEVNE 16
 ||||:|||||
 Db 1 PPFEMKPEVNE 9

Search completed: March 3, 2003, 07:00:47
 Job time: 15 secs

GenCore version 5.1.1
 1993-2003 Copyright

using sw model

003, 06:37:39 / Search time 11.667 Seconds
 (without alignments)
 11,611 Million cell pfms/sec

43.4%

REPRESK 16

3.34x10⁵

3.34x10⁵ residues

typical chosen parameters 2770

1st 45 summaries

of 4 results predictably change to have a
 equal to the score of the result being printed,
 1/5th of the total score distribution

SUMMARIES

PR	ID	Description
1	A28144	ribosomal protein
2	A32971	heparin-binding le
3	A42089	transcription fact
4	A45681	orf 61.1 - phage T
5	A33716	2S albumin large c
6	A29719	thymic humoral fac
7	A32693	ribosomal protein
8	A41383	32K variable histo
9	A29719	2S albumin large c
10	A32971	heparin-binding le
11	A42089	transcription fact
12	A45681	orf 61.1 - phage T
13	A33716	2S albumin large c
14	A29719	thymic humoral fac
15	A32693	ribosomal protein
16	A41383	32K variable histo
17	A29719	2S albumin large c
18	A32971	heparin-binding le
19	A42089	transcription fact
20	A45681	orf 61.1 - phage T
21	A33716	2S albumin large c
22	A29719	thymic humoral fac
23	A32693	ribosomal protein
24	A41383	32K variable histo
25	A29719	2S albumin large c
26	A32971	heparin-binding le
27	A42089	transcription fact
28	A45681	orf 61.1 - phage T
29	A33716	2S albumin large c
30	A29719	thymic humoral fac
31	A32693	ribosomal protein
32	A41383	32K variable histo
33	A29719	2S albumin large c
34	A32971	heparin-binding le
35	A42089	transcription fact
36	A45681	orf 61.1 - phage T
37	A33716	2S albumin large c
38	A29719	thymic humoral fac
39	A32693	ribosomal protein
40	A41383	32K variable histo
41	A29719	2S albumin large c
42	A32971	heparin-binding le
43	A42089	transcription fact
44	A45681	orf 61.1 - phage T
45	A33716	2S albumin large c

30	19	23.2	15	2	I49407
31	19	23.2	16	2	S65703
32	19	23.2	16	2	A60929
33	19	23.2	16	2	PH1351
34	18	22.0	7	2	A44428
35	18	22.0	10	1	A428PC
36	18	22.0	10	2	S65388
37	18	22.0	10	2	F41839
38	18	22.0	10	2	S77930
39	18	22.0	10	2	S43722
40	18	22.0	11	2	S23173
41	18	22.0	12	2	S65409
42	19	22.0	12	2	A44874
43	18	22.0	13	2	A28053
44	18	22.0	13	2	C53275
45	18	22.0	14	2	A39703

ALIGNMENTS

RESULT 1
 A28144
 Ribosomal protein S27a - bovine (fragment)
 C:Species: Bos primigenius taurus (cattle)
 C:Date: 28-Aug-1989 #sequence_revision 26-Aug-1989 #text change 21-Feb-2000
 C:Accession: A28144
 R:Redman, K.L.; Rechsteiner, M.
 J. Biol. Chem. 263, 4926-4931, 1988
 A:Title: Extended reading frame of a ubiquitin gene encodes a stable, conserved, larva
 A:Reference number: A28144; MUID:881696.9; PMID:2832412
 A:Accession: A28144
 A:Molecule type: protein
 A:Residues: 1-16 (RED)
 C:Superfamily: ubiquitin / rat ribosomal protein S27a; ribosomal protein S27a for long
 C:Keywords: protein biosynthesis

Query Match: 15.41; Score 33.5; LB 2; Length 16;
 Best Local Similarity 57.11; Pred. No. 1.4e-02;
 Matches 8; Conservative 2; Mismatches 1; Indels 3; Gaps 1;

QY 4 KKKKKYS---PSYS 14
 |||||
 DB 2 KKKKKSYTTPKN 15

RESULT 2
 A32971
 heparin-binding lectin - human (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 12-Dec-1987 #sequence_revision 12-Dec-1987 #text change 12-Feb-1997
 C:Accession: A32971
 F.Klenke 353; E. Gabus, H.C.
 Biochemistry 28, 6531-6538, 1989
 A:Title: Heparin binding lectin from human placenta, purified and partial sequence
 A:Reference number: A32971; MUID:890901.7; PMID:2749011
 A:Accession: A32971
 A>Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-15 (YOH)
 C:Keywords: heparin binding

Query Match: 24.11; Score 59; LB 2; Length 15;
 Best Local Similarity 54.98; Pred. No. 7.3e-02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KKKKKYSPPK 13
 |||||
 DB 4 PATKKVSPPK 14

RESULT 3
 A42089

transcription factor 1, POU protein, alternative splice form fruit fly *Drosophila melanogaster*
 CSpecies: *Drosophila melanogaster*
 CDate: 04-Mar-1994 #sequence_revision 1 to 2 1994 #text_change 00-Mar-1994
 CAccession: A42089
 CTitle: Twin of POU, a two amino acid difference in the POU home domain. Hittingbird
 CRef: 68, 491-500, 1993
 AReference number: A42089; MIM:60154665; PMID:1346754
 AAccession: A42089
 AStatus: preliminary
 A.Molecule type: PNA
 AResidues: 1-10 <TRE>
 ACross-references: GR:892071; NID:Q245519; PID:Q245518
 A.Motif sequence extracted from NCBI database: GATGAG AG, 67, NID:Q245519, NID:Q245518
 CGenetics:
 AGenetic: FlyBase: FLYBASE:FBgn0004416
 ACross-references: FlyBase: FBgn0004416
 Query Match 30.74, Score 27, PP 2, Length 10
 Best Local Similarity 52.61, Pred. No. 7, 100%
 Matches 5, Conservative 0, Mismatches 1, Indels 0, Gaps 0
 CY 5 GPKPKPKS 10
 DB 1 GPKPKPKS 9
 RESULT 4
 G45681
 CTitle: phage T6 (fragments)
 CSpecies: phage T6
 CDate: 03-Sep-1993 #sequence_revision 1 to 2 1993 #text_change 12-Sep-1994
 CAccession: G45681
 CTitle: H.B.; Stormo, G.D.; Dyson, R.L.; Alberts, B.M.
 J. Virol. 67, 2305-2316, 1993
 AReference number: A45681; MIM:60154665; PMID:841243
 AAccession: G45681
 AStatus: preliminary
 A.Molecule type: nucleic acid
 AResidues: 1-16 <EN>
 A.Motif sequence extracted from NCBI database: GATGAG AG, 67, NID:Q245519, NID:Q245518
 Query Match 31.71, Score 27, PP 2, Length 10
 Best Local Similarity 71.41, Pred. No. 1, 100%
 Matches 5, Conservative 1, Mismatches 1, Indels 0, Gaps 0
 CY 4 KPKPKS 10
 DB 4 KPKPKS 10
 RESULT 5
 2S albumin large chain (1 and 2) nII - rape (fragments)
 N.Altitude names: 2S albumin large chain nII
 CSpecies: *Brassica napus* (rape)
 CDate: 11-Dec-1994 #sequence_revision 1 to 2 1995 #text_change 11-Aug-1994
 CAccession: S09716; S09718; S09717
 R.Monsalvo, P. I.; Moroder, A.; L. Lopez-Otin, C.; Rodriguez, R.
 FEBS Lett. 353, 200-212, 1994
 AReference number: S09716; S09718; S09717; MIM:1243174; PMID:1243171
 AAccession: S09716
 A.Molecule type: PNA
 AResidues: 1-9, 10, 13 <MON>
 AExperimental source: seed
 A.Motif sequence extracted from NCBI database: GATGAG AG, 67, NID:Q245519, NID:Q245518
 A.Molecule type: PNA
 AResidues: 1-9, 10, 13 <MON>
 AExperimental source: seed
 AAccession: S09716

A.Molecule type: protein
 AResidues: 1-9, 10, 13 <MON>
 AExperimental source: seed
 Query Match 30.74, Score 27, PP 2, Length 10
 Best Local Similarity 71.41, Pred. No. 1, 100%
 Matches 5, Conservative 1, Mismatches 1, Indels 0, Gaps 0
 CY 5 GPKPKPKS 12
 DB 3 GPKPKPKS 13
 RESULT 6
 A28719
 CTitle: human factor gamma 2 bovine (fragment)
 CSpecies: *Human factor gamma 2 bovine*
 CDate: 30-Sep-1989 #sequence_revision 1 to 2 1993 #text_change 18-Jun-1994
 CAccession: A28719
 CTitle: V. Bachner, V. Pecht, M. Trainin, N.
 Biochemistry 17, 4068-4071, 1988
 AReference number: A28719; MIM:60154665; PMID:321994
 AAccession: A28719
 A.Molecule type: protein
 AResidues: 1-8 <BUR>
 Query Match 29.31, Score 24, PP 2, Length 10
 Best Local Similarity 100.0%, Pred. No. 2, 100%
 Matches 4, Conservative 0, Mismatches 0, Indels 0, Gaps 0
 CY 1 GPKPK 4
 DB 3 GPKPK 6
 RESULT 7
 S36893
 CTitle: Mytilus edulis (fragment)
 CSpecies: *Mytilus edulis*
 CDate: 13-Sep-1993 #sequence_revision 1 to 2 1993 #text_change 13-Jun-1994
 CAccession: S36893
 R.Chara, N.; Kimura, M.; Higashi, Y.; Yamada, T.
 FEBS Lett. 331, 1-14, 1993
 AReference number: S36893; MIM:60154665; PMID:841243
 AAccession: S36893
 AStatus: preliminary
 A.Molecule type: protein
 AResidues: 1-15 <OH>
 Query Match 29.31, Score 24, PP 2, Length 10
 Best Local Similarity 100.0%, Pred. No. 2, 100%
 Matches 4, Conservative 0, Mismatches 0, Indels 0, Gaps 0
 CY 1 GPKPK 6
 DB 4 GPKPK 9
 RESULT 8
 C4183
 CTitle: Chlamydia trachomatis
 CSpecies: *Chlamydia trachomatis*
 CDate: 28-May-1993 #sequence_revision 1 to 2 1993 #text_change 18-Jun-1994
 CAccession: C4183; S4183
 J. Bacteriol. 173, 7045-7048, 1991
 AReference number: C4183; S4183; MIM:1243174; PMID:1243171
 AAccession: C4183
 AStatus: preliminary
 A.Molecule type: protein

QY 5 KKKKKSPK 13
| | | | |
DB 8 KTKKKPQR 16

RESULT 14

PH0137
T-cell receptor beta chain V-D-J region MS20 - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 01-Nov-1991 #Sequence_revision: 01 Nov 1991 #ext_change: 00-May-1997
C:Accession: PH0137
R:Martin, R.; Howell, M.D.; Jaraquemada, D.; Flierlage, M.; Richert, J.; Brostoff, S.; Loefer, J. Exp. Med. 173, 19-24, 1991
A:Title: A myelin basic protein peptide is recognized by cytotoxic T cells in the context of H-2D^b
A:Reference_number: PH0137; MIM:6106843; PMID:1702137
A:Accession: PH0137
A:Molecule_type: mRNA
A:Residues: 1-16 <MAR>
C:Keywords: T cell receptor

Query Match: 20.6%, Score 21, DB 2, Length 16;
Best Local Similarity: 66.7%, Pred. No. 6.8e+03;
Matches: 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 7 KKKSPS 12
| | | | |
DB 7 KKDSPS 12

RESULT 15

154379
gene NF2 protein - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 01-Nov-1991 #Sequence_revision: 01 Nov 1991 #ext_change: 01 Jul 2000
C:Accession: 154379
R:Arai, E.; Ikeuchi, T.; Nakamura, Y.
Hum. Mol. Genet. 3, 947-949, 1994
A:Title: Characterization of the translocation breakpoint in chromosome 22q12.2 in a patient with neurofibromatosis type 2
A:Reference_number: 154379; MIM:6034750; PMID:7951241
A:Accession: 154379
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule_type: DNA
A:Residues: 1-9 <RES>
A:Cross_references: GB 972941, NID 3861512, FICH:AA014190 1; PIN:G4261890
C:Genetics:
A:Gene: GDB:NF2
A:Cross_references: GDB:120232; OMIM:101090
A:Map position: 22q12.2 22q12.2

Query Match: 24.4%, Score 20, DB 2, Length 9;
Best Local Similarity: 57.1%, Pred. No. 2.8e+05;
Matches: 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 5 KKKKKSP 11
| | | | |
DB 3 KKKKASP 9

Search completed: March 3, 2003, 10:46:07
Job time: 11.6667 secs


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CC  or send an email to: us09-214-913-40@fda.gov
CC  EMBL: J03653, AAA44685.1,
DR  HIV; J03653; TAI50Y1.
KW  Transcription regulation, Activation, RNA binding, Nuclear protein,
KW  Aids
FT  NON TER 1 1
SQ  SEQUENCE 14 AA; 1455 MW; 3A0C130BFF2D0AAB CRC64;
Query Match
Best Local Similarity 28.6%; Pct. ID: 1.1e+05; Length 14;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 2 GPKK 5
DB 11 GPKK 14
RESULT 14
UH09 RAT STANDARD; PRT; 8 AA.
AC P56575;
DT 15-DEC-1998 (rel. 37, Created)
DT 15-DEC-1998 (rel. 37, Last sequence update)
DT 15-DEC-1998 (rel. 37, Last annotation update)
DE Unknown protein from 2P-page of heart tissue (Spot P9) (Fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota, Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi;
OC Mammalia; Eutheria, Rodentia, Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE.
PC STRAIN=Wistar; TISSUE=Heart;
RA Li X. P., Plessner K. P., Scheler C., Regitz-Zagrosek V., Salikov J.,
RA Jungblut P. R.;
FC Submitted (FSP-1388) to the SWISS-PROT data bank.
CC 1 MISTELARFES CM THE IP-DEL THE IP-PEWINE IT OF THIS UNFPMW
CC PROTEIN IS: 8.9, ITS MW IS: 42 kDa.
FT NON TER 8
SQ SEQUENCE 8 AA; 1029 MW; 9E075A6C4140B05 CRC64;
Query Match
Best Local Similarity 28.6%; Pct. ID: 1.1e+05; Length 8;
Matches 2; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
QY 5 KKKKSP 11
DB 1 QKKKSP 7
RESULT 15
RPP VIPAS STANDARD; PRT; 10 AA.
AC P31351;
DT 01-JUN-1993 (rel. 26, Created)
DT 01-FEB-1994 (rel. 28, Last sequence update)
DT 01-FEB-1994 (rel. 28, Last annotation update)
DE Bradykinin-potentiating peptide (Angiotensin-converting
DE enzyme inhibitor)
OS Vipera aspis (Aspic viper).
OC Eukaryota, Metazoa, Chordata, Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria, Squamata; Serpentes; Colubroidea;
OC Viperidae; Viperinae; Vipera.
OX NCBI_TaxID=8706;
RN [1]
RP SEQUENCE.
PC TISSUE=Venom;
RC MFTUINE=0047-14; PubMed=2169439;
RX Kowori Y., Sugihara H.;
RT "Characterization of a new inhibitor for angiotensin converting
RT enzyme from the venom of Vipera aspis aspis.";
PL Int. J. Biochem. 22:767-771(1990).
CC 1 FUNCTION. THIS PEPTIDE BOTH INHIBITS THE ACTIVITY OF THE

```

```

CC  ANGIOTENSIN CONVERTING ENZYME AND ENHANCES THE ACTION OF
CC  BRADYKININ BY INHIBITING THE KINASES THAT INACTIVATE IT.
CC  IT ACTS AS AN INHIBIT OF HYPERSENSITIVE AGENT.
DR  PIR; A60377; XASNEC.
KW  Hypersensitive agent, Venom.
FT  MOD RES 1 1
SQ  SEQUENCE 10 AA; 1050 MW; 3FA2D0D0D0D0D0D0 CRC64;
Query Match
Best Local Similarity 100.0%; Pct. ID: 2.1e+03; Length 10;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 GPK 4
DB 5 GPK 7
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Job time : 6.66667 secs

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```

DE Adenylate Kinase (E.C.2.7.1.37) (Fragment)
OS Mus musculus (Mouse)
--
FA 100.000000 (1)
OC Mammalia; Eutheria; Rodentia; Muridae; Murinae; Mus
CX Mmu.Taxid-10000.
RN 100.000000 (1)
RP SEQUENCE FROM N.A.
RA Singh B., Lin A., Wu Z. C., Gupta R.S.
RT "Gene Structure for Adenosine Kinase in Chinese Hamster and Human:
RT High Frequency Mutants of CHO Cells Involving Deletions of Several
RT Introns and Exons."
RL DMA Cat. Piv. 2.6 (2001).
DP EMBL; AF14063; AAK01661.1; -
KW Kinase; Transferase.
FT NON_TER 14
SQ SEQUENCE 14 AA: 1426 MW: 27933.765/DNA2/ CPG64;

Query Match 34 14; Score 28; DP 11; Length 14;
Best Local Similarity 66.71; Pct. Id. 7.4e+02;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 PDPYVYVYV 9
DB 5 DEEPRFFR 13

RESULT 3
Q47612 PRELIMINARY; PRT; 15 AA.
AC Q47612;
DT 01-NOV-1996 (TRENBERG 01, Created)
DT 01-NOV-1996 (TRENBERG 01, Last sequence update)
DT 01-DEC-2001 (TRENBERG 13, Last annotation update)
DE Rpsd protein (Fragment)
GN Rpsd
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID:562;
RN 100.000000 (1)
RP SEQUENCE FROM N.A.
RC STRAIN: 12, 72343, FHM-1-1894866.
RX MERLIN 82767243, FHM-1-1894866.
RA Schrier J., Iseno S., Gumberidge A.G., Iseno K.
RT "Unstable mutations caused by regional tandem multiplications in the
RT gene for ribosomal protein S4 show thermosensitivity in Escherichia
RT coli."
RL MGI Gen. Genet. 199.245-270 (1995).
DR EMBL; M29924; AAM24591.1; -
FT NON_TER 1
SQ SEQUENCE 15 AA: 1545 MW: 74810.444/PROT/ CPG64;

Query Match 31 78; Score 20; DP 2; Length 15;
Best Local Similarity 33.63; Pct. Id. 1.4e+03;
Matches 0; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 4 KKKKKKSPKSS 15
DB 1 EVAKKSPVKAS 12

RESULT 4
Q50268 PRELIMINARY; PRT; 14 AA.
AC Q50268;
DT 01-NOV-1996 (TRENBERG 01, Created)
DT 01-JAN-1999 (TRENBERG 09, Last sequence update)
DT 01-DEC-2001 (TRENBERG 14, Last annotation update)
DE RPL16 protein (Fragment)
GN RPL16
OS Phytoplasma sp.
OC Bacteria; Eubacteria; Rhodospirillum rubrum; Rhodospirillaceae;
OC Actinoplasmatales; Rhodospirillum rubrum; Rhodospirillum.

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CX NCBI_TaxID 2155;
RN 100.000000 (1)
RP SEQUENCE FROM N.A.
RA Lim P.O., Sears R.
RT "RNA sequence of the ribosomal protein genes rpl2 and rpl9 from a
RT plant-pathogenic mycoplasma-like organism."
RL FWS Microbiol. Lett. 84:71-74 (1991).
RN 100.000000 (1)
RP SEQUENCE FROM N.A.
RA MERLIN-3221055; FWS-1556079;
RA Lim P.O., Sears R.
RT "Evolutionary relationships of a plant pathogenic mycoplasma-like
RT organism and Actinoplasmata lial with deduced from two ribosomal protein
RT gene sequences."
RL J. Bacteriol. 174:2635-2641 (1992).
DR EMBL; M74770; AAM75331.1; -
FT NON_TER 14
SQ SEQUENCE 14 AA: 1870 MW: 8703153/PROT/ CPG64;

Query Match 30 57; Score 25; DP 2; Length 14;
Best Local Similarity 36.48; Pct. Id. 2.1e+03;
Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 3 DKKKKKSPSK 13
DB 4 PDKTKRPR 14

RESULT 5
Q84271 PRELIMINARY; PRT; 8 AA.
AC Q84271;
DT 01-NOV-1996 (TRENBERG 01, Created)
DT 01-NOV-1996 (TRENBERG 01, Last sequence update)
DT 01-DEC-2001 (TRENBERG 13, Last annotation update)
DE L1 protein (Fragment)
OS Human papillomavirus type 19.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID:10608;
RN 100.000000 (1)
RP SEQUENCE FROM N.A.
RX MERLIN-3221055; FWS-1556079;
RA Krutke J., Kraus J., Deltus H., Chow L., Hocker T.R., Hinet T.
RT "Genetic relationship among human papillomaviruses associated with
RT benign and malignant tumors of patients with epidermodysplasia
RT verruciformis."
RL J. Gen. Virol. 69:3591-3603 (1997).
DR EMBL; D06204; F0000142.1; -
FT NON_TER 1
SQ SEQUENCE 8 AA: 987 MW: 7943240/240/21AB CPG64;

Query Match 35 38; Score 34; DP 12; Length 8;
Best Local Similarity 17.13; Pct. Id. 4.7e+04;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 GKKKKK 8
DB 1 GKKKKK 7

RESULT 6
Q61574 PRELIMINARY; PRT; 12 AA.
AC Q61574;
DT 01-NOV-1996 (TRENBERG 01, Created)
DT 01-NOV-1996 (TRENBERG 01, Last sequence update)
DT 01-DEC-2001 (TRENBERG 13, Last annotation update)
DE Hypothetical 1.4 kDa protein (Fragment)
OS Ostertagia ostertagi.
FT NON_TER 12
SQ SEQUENCE 12 AA: 1200 MW: 120000000/PROT/ CPG64;

Query Match 35 38; Score 34; DP 12; Length 8;
Best Local Similarity 17.13; Pct. Id. 4.7e+04;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 GKKKKK 8
DB 1 GKKKKK 7

RESULT 6
Q61574 PRELIMINARY; PRT; 12 AA.
AC Q61574;
DT 01-NOV-1996 (TRENBERG 01, Created)
DT 01-NOV-1996 (TRENBERG 01, Last sequence update)
DT 01-DEC-2001 (TRENBERG 13, Last annotation update)
DE Hypothetical 1.4 kDa protein (Fragment)
OS Ostertagia ostertagi.
FT NON_TER 12
SQ SEQUENCE 12 AA: 1200 MW: 120000000/PROT/ CPG64;

```



```

QY 4 PVPVPSK 14
DB 7 KPEPTTSPK 16

RESULT 11
Q920X9 PRELIMINARY; PRT; 10 AA.
ID Q920X9
AC Q920X9;
DT 01-MAY-2000 (TREMURel. 13, Created)
DT 01-MAY-2000 (TREMURel. 13, Last sequence update)
DE Large T antigen (Fragment)
OS Polyomavirus JC.
CC Viruses; dsDNA viruses, no RNA stage, Polyomaviridae.
OX NCBI_TaxID=10632;
PN [1]
FP SEQUENCE FROM N.A.
RC STRAIN=BCN16;
RA Bofill-Mas S., Pina S., Girones R.;
RT "Documenting the epidemiologic patterns of polyomaviruses in human
    populations by studying their presence in urban sewage."
PL Appl Environ Microbiol 69:239-245(2003)
DR EMBL; AF119347; AAF24100.1; -
FT NON_TER 1
SQ SEQUENCE 10 AA; 1167 MW; 40DA9771A32763 CRC64;

Query Match
Best Local Similarity 55.6%; Score 23; DP 12; Length 10;
Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 5 PVPVPSK 13
DB 2 KPEPTTSPK 10

RESULT 12
Q920X5 PRELIMINARY; PRT; 10 AA.
ID Q920X5
AC Q920X5;
DT 01-MAY-2000 (TREMURel. 13, Created)
DT 01-MAY-2000 (TREMURel. 13, Last sequence update)
DE Large T antigen (Fragment)
OS Polyomavirus JC.
CC Viruses; dsDNA viruses, no RNA stage, Polyomaviridae.
OX NCBI_TaxID=10632;
PN [1]
FP SEQUENCE FROM N.A.
RC STRAIN=BCN16;
RA Bofill-Mas S., Pina S., Girones R.;
RT "Documenting the epidemiologic patterns of polyomaviruses in human
    populations by studying their presence in urban sewage."
PL Appl Environ Microbiol 69:239-245(2003)
DR EMBL; AF119347; AAF24100.1; -
FT NON_TER 1
SQ SEQUENCE 10 AA; 1167 MW; 40DA9771A32763 CRC64;

Query Match
Best Local Similarity 55.6%; Score 23; DP 12; Length 10;
Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 5 PVPVPSK 14
DB 2 KPEPTTSPK 10

RESULT 13
Q920X3 PRELIMINARY; PRT; 10 AA.
ID Q920X3
AC Q920X3;
DT 01-MAY-2000 (TREMURel. 13, Created)
DT 01-MAY-2000 (TREMURel. 13, Last sequence update)
DE Large T antigen (Fragment)
OS Polyomavirus JC.
CC Viruses; dsDNA viruses, no RNA stage, Polyomaviridae.
OX NCBI_TaxID=10632;
PN [1]
FP SEQUENCE FROM N.A.
RC STRAIN=BCN16;
RA Bofill-Mas S., Pina S., Girones R.;
RT "Documenting the epidemiologic patterns of polyomaviruses in human
    populations by studying their presence in urban sewage."
PL Appl Environ Microbiol 69:239-245(2003)
DR EMBL; AF119347; AAF24100.1; -
FT NON_TER 1
SQ SEQUENCE 10 AA; 1167 MW; 40DA9771A32763 CRC64;

Query Match
Best Local Similarity 55.6%; Score 23; DP 12; Length 10;
Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 5 PVPVPSK 13
DB 2 KPEPTTSPK 10

RESULT 14
Q920X1 PRELIMINARY; PRT; 10 AA.
ID Q920X1
AC Q920X1;
DT 01-MAY-2000 (TREMURel. 13, Created)
DT 01-MAY-2000 (TREMURel. 13, Last sequence update)
DE Large T antigen (Fragment)
OS Polyomavirus JC.
CC Viruses; dsDNA viruses, no RNA stage, Polyomaviridae.
OX NCBI_TaxID=10632;
PN [1]
FP SEQUENCE FROM N.A.
RC STRAIN=BCN16;
RA Bofill-Mas S., Pina S., Girones R.;
RT "Documenting the epidemiologic patterns of polyomaviruses in human
    populations by studying their presence in urban sewage."
PL Appl Environ Microbiol 69:239-245(2003)
DR EMBL; AF119347; AAF24100.1; -
FT NON_TER 1
SQ SEQUENCE 10 AA; 1167 MW; 40DA9771A32763 CRC64;

Query Match
Best Local Similarity 55.6%; Score 23; DP 12; Length 10;
Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 5 PVPVPSK 13
DB 2 KPEPTTSPK 10

RESULT 15
Q920W9 PRELIMINARY; PRT; 10 AA.
ID Q920W9
AC Q920W9;
DT 01-MAY-2000 (TREMURel. 13, Created)
DT 01-MAY-2000 (TREMURel. 13, Last sequence update)
DE Large T antigen (Fragment)
OS Polyomavirus JC.
CC Viruses; dsDNA viruses, no RNA stage, Polyomaviridae.
OX NCBI_TaxID=10632;
PN [1]
FP SEQUENCE FROM N.A.
RC STRAIN=BCN16;
RA Bofill-Mas S., Pina S., Girones R.;
RT "Documenting the epidemiologic patterns of polyomaviruses in human
    populations by studying their presence in urban sewage."
PL Appl Environ Microbiol 69:239-245(2003)
DR EMBL; AF119347; AAF24100.1; -
FT NON_TER 1
SQ SEQUENCE 10 AA; 1167 MW; 40DA9771A32763 CRC64;

Query Match
Best Local Similarity 55.6%; Score 23; DP 12; Length 10;
Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 5 PVPVPSK 13
DB 2 KPEPTTSPK 10

```




XX PS Claim 11; Page 70; 75pp; English.

XX CC The present peptide sequence represents a specifically claimed membrane

XX CC binding element. The invention relates to a soluble derivative (A) of a

XX CC soluble polypeptide (B), which comprises at least one heparin-binding

XX CC membrane-binding elements (MBE) of low membrane affinity covalently

XX CC associated with the MBE interact, independently and with thermodynamic

XX CC additivity, with components of collagen or artificial membranes exposed

XX CC to extracellular fluids (A) are used to treat disorders treatable with

XX CC (II) itself, specifically inflammation or any other complement-related

XX CC disorder (e.g. neurological disease, graft rejection, myocardial

XX CC infarction, sepsis, rheumatoid arthritis and many others), including

XX CC application to immobilizing devices and rheumatoid disease, but also to

XX CC treat allergy, induce weight loss, to treat ischaemia or asthma and as

XX CC immunomodulators for treating multiple sclerosis (A) are administered

XX CC orally, topically, by injection or inhalation at a 0.1-10 (preferably

XX CC 0.1-1) mg/kg/day

XX SQ Sequence 16 AA;

Query Match 100.0%; Score 82; DB 13; Length 16;

Best local similarity 100.0%; Pred No 1 seqs;

Matches 10; Conservation 0; Mismatches 0; Indels 0; Gaps 0;

CY 1 DQPKKKKKKSPSKSK 16

DB 1 DQPKKKKKKSPSKSK 16

RESULT 2

AAV58858

ID AAY58858 standard; Peptide; 16 AA.

XX AC AAY58858;

XX DT 08-MAY-2000 (first entry)

XX DF Membrane binding element used in anti angiogenic polypeptide.

XX FW Anti-angiogenic, angiogenesis inhibition, membrane binding element,

XX FW cancer, tumor, therapy.

XX OS Synthetic.

XX PN WC2000094052 A2.

XX PD 27 JAN 2000.

XX PF 16-JUL-1997; 94WO-GB00292

XX PR 16-JUL-1998; 98GB 0015505.

XX PA (ADPP-) ADPPOTTECH PIC.

XX PI Smith RAG, Bright OR, Steward M, Cox VP;

XX WPI; 2000 192406/16.

XX CC Now soluble derivative of anti angiogenic polypeptide useful for

XX CC treatment of primary secondary tumors, contains a soluble polypeptide

XX CC membrane-binding elements for targeting

XX CC Claim 12, Page 10, 36pp; English.

XX CC The present sequence is a claimed example of a lysine rich peptide

XX CC membrane binding element (MBE) that can be utilised in novel

XX CC soluble derivatives (A) of anti angiogenic polypeptides of the

XX CC invention (B). The peptide (A) is a polypeptide with low

XX CC membrane affinity that are covalently attached to a soluble

XX CC anti angiogenic polypeptide (B) as a means of targeting the

XX CC peptide, fragments of related proteins containing lysine

XX CC binding, fragments of collagen or fibrin, neutralising

XX CC antibodies against receptors for anti angiogenic mediators, and

XX CC antagonists of integrins involved in angiogenesis. The MBEs

XX CC interact independently with thermodynamic additivity, with

XX CC components of the vascular endothelium (II) provide targeted

XX CC delivery of the anti angiogenic polypeptide (B) to cell receptors and

XX CC sites of action and increase the local concentration and reduce the size

XX CC and therefore increase the local concentration and reduce the size

XX CC of adverse effects of the anti angiogenic element in the vasculature.

XX CC They are used in a claimed method of treatment of primary or

XX CC secondary tumour.

XX SQ Sequence 16 AA;

Query Match 100.0%; Score 82; DB 21; Length 16;

Best local similarity 100.0%; Pred No 1 seqs;

Matches 10; Conservation 0; Mismatches 0; Indels 0; Gaps 0;

CY 1 DQPKKKKKKSPSKSK 16

DB 1 DQPKKKKKKSPSKSK 16

RESULT 3

AB881240

ID AB881240 standard; peptide; 16 AA.

XX AC AB881240;

XX DT 20-AUG 2002 (first entry)

XX DE Antibacterial membrane binding peptide SEQ ID NO:7.

XX FW Antibacterial, glycopeptide, peptide, membrane-associated element,

XX FW bactericidal, inhibitory, activity, peptide, glycopeptide, bactericidal inhibition,

XX KW antibiotic.

XX OS Synthetic.

XX PN WC2000036502-A1.

XX PD 10 MAY 2002

XX PF 02 Nov 2001; 2001WO-GB04467.

XX PR 03-NOV-2000; 2000GB 0026024.

XX PA (UYCA-) UNIV CAMBRIDGE TECH SERVICES LTD.

XX PA (ADPP-) ADPPOTTECH LTD.

XX PI Cooper MA, Portley JP;

XX WPI; 2002-471404/40

XX PT Antibacterial compound, useful for the treatment of a bacterial

XX PT infection by e.g. gram positive or negative bacteria, comprises a

XX PT conjugate of glycopeptide and peptide membrane-associated element

XX CC Claim 7; Page 57; 64pp; English.

XX CC The present invention describes an antibacterial compound (II), comprising

XX CC a conjugate of glycopeptide and peptide membrane-associated element,

XX CC (I) comprises the formula V L W Y, where V is a glycopeptide moiety that

XX CC inhibits peptidoglycan biosynthesis in bacteria, L is a linking group

XX CC W is a peptide moiety associated with the glycopeptide moiety V, and Y is a

XX CC inactive element. Also described (II) a method of treating or preventing

XX CC a bacterial infection, comprising the administration of (I), and (3) use

XX CC of (I) in the manufacture of a medicament for the treatment of prevention

XX CC of a bacterial infection. (I) are used in the manufacture of a medicament

XX CC for the treatment of prophylaxis of a bacterial infection in a human or

XX CC animal body, including both the oral, parenteral and topical routes

XX CC including Mycobacterium sp., Enterobacter sp., Pseudomonas sp.,

XX CC Streptococcus sp., Vibrio sp., Klebsiella sp., Shigella sp.,

XX CC S. flexneris sp., Shigella sp., E. coli and of a bacterium of

[illegible]

33; store 82; 19.0; Larch 16;

```

0.00; Pred. No. i.e. 0;
0.00; Mismatched 0; Inbols 0; Gaps 0;

```

A
C
E

1

thrombotic disease; inhibition;

Public Performance

10

oligonucleotide's binding to the low affinity receptor is useful for treating the symptoms related and without approved treatment of the cellular

10

[illegible]

Sequence in AA.

Figure 6

Category	Count	Percentage
Best Local Similarity	100.00	100.00%
Best Overall Similarity	100.00	100.00%
Matches	157	100.00%
Conservative	0	0.00%
Aggressive	0	0.00%

New soluble derivative of anti-oncogenic polypeptide useful for treatment of primary or secondary tumors, including targeted membrane-binding elements for targeting

Claim 12; Page 32; 36pp; English.

The present sequence is a claimed example of a lymph node, lymphoid membrane binding element (MSE) that can be utilized to deliver soluble derivatives (1) of anti angiogenic polypeptides of the invention. (1) comprise 2 or more heterologous parts with low membrane affinity that are covalently attached to a soluble anti angiogenic polypeptide, such as the soluble form of plasminogen, fragments of related proteins containing kinase domains, fragments of collagen or fibronectin, neurotensin, antagonists of integrins involved in angiogenesis, the VEGF antagonist of integrins involved in angiogenesis, the VEGF inhibitor interferon- γ with endothelial activity, with components of the vascular endothelium. (1) provide targeted delivery of the anti angiogenic polypeptide to cell membrane and sites of active angiogenesis, particularly the vascular endothelium, and therefore increase the local concentration and reduce the risk of adverse effects of active polypeptides that are anti angiogenic. They are used in a claimed method of treatment of primary and secondary tumors.

Sequence in AA.

Figure 6

Category	Count	Percentage
Best Local Similarity	100.00	100.00%
Best Overall Similarity	100.00	100.00%
Matches	157	100.00%
Conservative	0	0.00%
Aggressive	0	0.00%

Best Local Similarity 100.0%; Pred. No. 8e-05;
Matches 10; Mismatches 0; Indels 0; Gaps 0;

CY 1 DGPFFFFFFPKSS 15
||||| ||||| |||||
DB 1 DGPFFFFFKSPSS 15

RESULT 7

AAW45882
ID AAW45882 standard; peptide, 14 AA.

XX AC AAW45882;

XX XX 20-JUN-1998 (first entry)

XX XX Peptide membrane binding element.

XX XX Membrane binding element; thrombotic disease; inflammation;

XX XX Complement-related disease; soluble peptide.

XX OS Synthetic.

XX XX WO9802454-A2.

XX XX 22-JAN-1998.

XX XX 08-JUL-1997; 97WO-EP03715.

XX XX 15-JUN-1996; 96GR-0014871.

XX XX (ADPR-) ADPROTECH PLC.

XX XX Sodi I, Mossakowska PFI, Smith RAG;

XX XX WPI; 1998-110524/10.

XX XX Derivatives of soluble poly-peptides bonded to low affinity membrane binding groups - useful for treating complement related and thrombotic diseases, providing improved localisation at cellular membranes

XX Claim 11; Page 70; 75pp; English.

XX The present peptide sequence represents a specifically claimed membrane binding element. The invention relates to a soluble derivative (A) of a stable polypeptide (P), which exhibits at least 50% homology with membrane binding element (MPE) of low membrane affinity. MPE is associated with (1) MPE insert, independently and with thermodynamic activity, with components of cellular or artificial membranes exposed to extracellular fluids. (A) are used to treat disorders treatable with (1) MPE, specifically inflammation, e.g. any other diseases related to infection, e.g. thrombotic diseases, graft rejection, myocardial infarction, peris, rheumatoid arthritis and many others, including application to inducing desensitisation and immunologic disease, for use to treat allergy, induce weight loss, to treat leukaemia or asthma and as immunomodulators for treating multiple sclerosis. (A) are administered orally, subcutaneously, by injection, intravenously or intraperitoneally 0.1-100 mg/kg/day.

XX Sequence 14 AA;

Query March 93, Score 42, SE 13, Length 14;
Pos: 100 (similarity) 90.94, Pred 96.16;
Matches 10; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

CY 1 DGPFFFFFFPKSS 15

DB 1 DGPFFFFFKSPSS 15

RESULT 8

ABB91241

CY 1 DGPFFFFFFPKSS 15
||||| ||||| |||||
DB 1 DGPFFFFFKSPSS 15

RESULT 6

ABB81237
ID ABB81237 standard; peptide, 16 AA.

XX AC ABB81237;

XX DT 20 AUG 2002 (first entry)

XX XX Anti-bacterial membrane binding peptide SEQ ID NO:4.

XX XX Anti-bacterial; glycopeptide; peptide membrane associating element;

XX XX Bacterial infection; vancomycin, peptidoglycan biosynthesis inhibition;

XX XX Antibiotic.

XX OS Synthetic.

XX PN WO200234612-A1.

XX XX 10-MAY-2002.

XX XX 02 NOV 2001, 2001WO GB04867.

XX XX 03-NOV 2000, 2000GB G025924.

XX XX (UYCA-) UNIV CAMBRIDGE TECH SERVICES LTD.

XX XX (ADPR-) ADPROTECH LTD.

XX XX Cooper WA, Rellay JE,

XX XX WPI; 2002-471492/50

XX XX Anti-bacterial compound, useful for the treatment of a bacterial infection by e.g. gram positive or negative bacteria, comprises a conjugate of glycopeptide and peptide membrane-associating element.

XX Claim 7; Page 57; 64pp; English.

XX The present invention describes an antibacterial compound (II), comprising a conjugate of glycopeptide and peptide membrane associating elements (I) as defined by the formula V: W-X, where W is a glycopeptide moiety that exhibits partial glycan biosynthesis inhibition, and X is a binding group. W is a peptide membrane associating element, and X is a membrane insertive element. Also described: (1) a method of treating or preventing a bacterial infection, comprising the administration of (I); and (2) use of (I) in the manufacture of a medicament for the treatment or prevention of a bacterial infection. (I) are used in the manufacture of a medicament for the treatment of a phylaxis of a bacterial infection in a human or animal body, including both the jaw peritone and gram negative bacteria including Mycobacterium sp., Enterococcus sp., Escherichia sp., Corynebacterium sp., Vibrio sp., Pseudomonas sp., Moraxella sp., Klebsiella sp., Haemophilus sp., Clostridium sp., Streptococcus sp., Actinomyces sp., Rhodospirillum sp., Salmonella sp., particularly antibiotic resistant bacterial strains. (I) are also useful as wound treatment agents to prevent adhesion of bacteria to matrix proteins, especially fibrinogen, exposed in wound tissue, and for prophylactic use in dental treatment as an alternative to, or in conjunction with, antibiotic prophylaxis. (I) has enhanced binding to bacterial membranes which have a higher ratio of phospholipids to sphingolipids than the eukaryotic membranes, and having a higher proportion of membrane associated biosynthetic proteins. Vancomycin shows an enhanced antimicrobial activity upon derivatization with (I), and is effective to treat the antibiotic resistant bacterial strains. ABB81241 to ABB81272 represent peptides given in the description of the present invention.

XX Sequence 16 AA;

Query March 93, Score 77, SE 23, Length 16,

100 14 AA.

17

100 14 AA.

100 14 AA.

100 14 AA.

100 14 AA.

100 14 AA.

100 14 AA.

100 14 AA.

100 14 AA.

100 14 AA.

100 14 AA.

100 14 AA.

100 14 AA.

100 14 AA.

100 14 AA.

100 14 AA.

100 14 AA.

100 14 AA.

100 14 AA.

100 14 AA.

100 14 AA.

100 14 AA.

100 14 AA.

100 14 AA.

100 14 AA.

100 14 AA.

RESULT 9

AAW45893

ID AAW45893 standard; peptide; 15 AA.

XX

AC AAW45893;

XX

DT 30-JUN-1998 (first entry)

XX

DE Peptide membrane binding element.

XX

KW Membrane binding element; thrombotic disease; solution protein;

XX

KW Complement-related disease; integral membrane protein; inflammation.

XX

OS Synthetic.

XX

PN WO9802454-A2.

XX

PD 22-JAN-1998.

XX

PF 08-JUL-1997; 97NO-EP03715.

XX

PR 15-JUL-1996; 96GB-0014871.

XX

PA (ADPR-) ADPROTECH PLC.

XX

PI Dodd I, Mossakowska DEJ, Smith FAG;

XX

DR WPI; 1998-110524/10.

XX

XX Derivatives of soluble polypeptides. Bonded to low affinity

PT

PT membrane binding proteins useful for treatment of thrombotic and

PT

PT thrombotic diseases, providing improved localization at cellular

PT

XX membranes

XX

PS Claim 21; Page 71; 75pp; English.

XX

XX The present peptide sequence represents a specifically claimed membrane

XX

XX binding element. The invention relates to a soluble derivative A of a

XX

XX soluble polypeptide (1), which comprises at least one functional

XX

XX membrane-binding element (MBE) of low membrane affinity, preferably

XX

XX associated with (1) MBE moiety, independently, and with the MBE

XX

XX to extracellular fluids. (A) are used to treat disorders treatable with

XX

XX (1) itself, specifically inflammation or any other complement-related

XX

XX disorder (e.g. neurological diseases, graft rejection, myocardial

XX

XX infarction, sepsis, rheumatoid arthritis and many others, including

XX

XX application to indwelling devices, and thrombotic diseases, but also to

XX

XX treat allergy, induce weight loss, to treat ischemic heart and/or

XX

XX immunomodulation for treating multiple sclerosis. A and derivatives

XX

XX orally, topically, by injection or inhalation at a dose of preferably

XX

XX 0.1 to 10 mg/kg/day.

XX

SQ Sequence 15 AA;

XX

Query Match

49.4%; Score 40.5; DB 19; Length 14;

Best Local Similarity 76.9%; Pred. No. 14;

Mismatches 10; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

Qy 1 DGVVKKKKKKKKKK 13

Db 3 DG-KKKKKKKKKKK 14

RESULT 10

AAW58865

ID AAW58865 standard; peptide; 15 AA.

XX

AC AAW58865;

XX

DT 08-MAY-2000 (first entry)

XX

DE Membrane binding element used in anti angiogenic polypeptides.

XX

PT diagnosis, prevention and treatment of ulcerative colitis
XX Example 3; Page 67; 134pp; English.
XX The invention provides a method for the diagnosis, prevention and
XX treatment of ulcerative colitis (UC) using histone H1-like antigen, a
XX porin antigen or a bacteroides antigen as a target antigen. The method
XX consists of identifying in a sample a signal affected by bacterial infection of
XX bowel disease (IBD) comprises: (1) obtaining a sample from the subject;
XX (2) contacting the sample with a histone H1-like antigen, or bacteroides
XX anti-neutrophil cytoplasmic antibody (pANCA) treatment fragment, to form
XX a complex of the histone H1-like antigen, or the pANCA treatment fragment,
XX fragment, and antibody to the histone H1-like antigen; and (3) detecting the
XX presence or absence of the complex; where the presence of the
XX complex indicates that the subject has the pANCA reactive histone
XX H1-like antigen, porin antigen and bacteroides antigen, or a signal on the
XX diagnosis, prevention and treatment of UC. The method can also be used
XX for identifying agents useful for treating UC. Sequence AAY57345-58
XX represent peptides spanning the human histone H1 gene product. These
XX were assayed for NANUC-1 and NANUC-2 binding to NANUC-1, pANCA and
XX peptides.
SQ Sequence 15 AA;
Query March 42 23; Score 47; 28 23; Length 15;
Best Local Similarity 58.3%; Pred. No. 19;
Matches 7; Conservative 2; Mismatches 3; Gaps 0;
QY 3 PPKKKKKSPKRS 14
||| ||||
DB 3 PPKSAKATPKPA 14
RESULT 14
AAY57345
ID AAY57345 standard; peptide; 15 AA.
XX AAY57345;
AC AAY57345;
XX
XX 13-JUN-2000 (first entry)
XX Human histone H1 pANCA-reactive peptide.
XX Ulcerative colitis; inflammatory bowel disease; porin antigen;
XX pANCA; perinuclear anti-neutrophil cytoplasmic antibody; human;
XX histone H1; isoform; NANUC-2.
XX
XX Homo sapiens.
XX
XX US6033864-A.
XX
XX 07-MAR-2000.
XX
XX 12-MAR-1998; 98US-0041889.
XX
XX 12-APR-1996; 96US-0057846.
XX
XX 11-APR-1997; 97US-0837058.
XX
XX (REGC) UNIV CALIFORNIA.
XX
XX Cohavy O, Braun C;
XX
XX WPI; 2000 255695/22.
XX
XX
XX Diagnosing ulcerative colitis or susceptibility, by detecting specific
XX formation between microbial porin antigen and perinuclear
XX anti-neutrophil cytoplasmic antibodies -
XX
XX Example 3; Column 30; 49pp; English.
XX
XX The invention provides a method for diagnosing ulcerative colitis in a
XX subject suspected of having inflammatory bowel disease. The method
XX comprises reacting a patient sample with a porin antibody that is

CC Immunologically reactive with pMNA (formation: anti-pMNA-ppHd
 CC cytoplasmic antibodies) and detecting formation of a Ag-AbrA complex
 CC as indicative of ulcerative colitis. The method is used to diagnose
 CC ulcerative colitis or susceptibility to it. Sequences AAY57341-351
 CC represent pMNA reactive peptides, derived from human histone H1.
 XX
 SQ Sequence 15 AA;

Query Match 49.54; Score 43, 12 21; Length 15;
 Best local similarity 59.34; Prod No. 19;
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 PRRKKKSPSKS 14
 |||||
 Zb 3 PRRKKKSPSKS 14

RESULT 15

AAR26821
 ID AAR26821 standard; peptide; 9 AA.

XX AC AAR26821;

XX DT 23 JAN 2001 (first entry)

XX DE Peptidic membrane binding element.

XX KW Organ perfusion, transplantation, storage, antiinflammatory;

XX KW immunosuppressive; vasotropic; complement activation inhibitor;

XX KW allograft rejection; ischaemia reperfusion injury.

XX OS Synthetic.

XX PN WC200051007-A1.

XX PD 14-SEP-2000.

XX PF 08-MAR-2000; 2000UO-UR00834.

XX PR 10-MAR-1999; 99GB-0005503.

XX PA (ADPP-) ADPPOTECH LTD.

XX PI Smith RAG, Pratt JR, Sacks SH;

XX DR WPI; 2000-601920/57.

XX PT Preparation for perfusing organ prior to transplantation or storage
 PT comprises soluble derivative of a soluble polypeptide- which comprises
 PT two heterologous membrane binding elements with low membrane affinity

PS Example 2; Page 20; 47pp, English.

XX The present invention relates to formulations and preparations for
 CC perfusing an organ prior to transplantation or storage. The preparation
 CC comprises a soluble derivative of a polypeptide, which has two or more
 CC heterologous membrane binding elements. The membrane binding elements are
 CC capable of interacting, independently and with thermodynamic additivity,
 CC with membrane components of the organ exposed to extracellular perfusion
 CC fluids, and a flush storage solution. The preparation exhibits
 CC antiinflammatory, immunosuppressive and vasotropic activity and works as
 CC a complement activation inhibitor and an inhibitor of cytotoxic T
 CC lymphocyte activity. The preparation is used for preparing an organ prior
 CC to transplantation or storage and for prevention, treatment or
 CC amelioration of a disease or disorder associated with inflammation,
 CC inappropriate complement activation or inappropriate activation of
 CC coagulant or thrombotic processes prior to, during or after
 CC transplantation or storage of an organ. The preparation is useful for
 CC treating hyperacute and acute allograft rejection of transplanted organs
 CC such as kidney, heart, liver or lungs, ischaemia-reperfusion injury in
 CC transplanted organs, xenograft rejection and corneal graft rejection. The
 CC present sequence represents a peptidic membrane binding element used in

XX as example of the preparation of the invention.
 XX Sequence 9 AA;

Query Match 49.54; Score 43, 12 21; Length 9;
 Best local similarity 77.81; Prod No. 7 Re:05;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 PRRKKKSP 11
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 Zb 1 PRRKKKSP 9

Search completed: March 3, 2003, 06:44:32
 Job time: 145 secs

Gen file version 1.1
10 1993 2003

us-ni sw model

3% 1445.44 : Search time = seconds
(with all alignments)
75.444 Million cell updates/sec

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ESPAAR 16

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3.421926 residues

print doset parameters: 1245

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Applications AA:

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ptdara/1/pubpa/1000 NEW PIR pep:

ptdara/1/pubpa/1000 NEW PIR pep:

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ptdara/1/pubpa/1000 NEW PIR pep:

of results predicted by chance to have a
equal to the score of the result being printed,
analysis of the total score distribution.

SUMMARIES

APP ID	Description
1	Sequence 53, Appl
2	Sequence 45, Appl
3	Sequence 46, Appl
4	Sequence 16, Appl
5	Sequence 44, Appl
6	Sequence 47, Appl
7	Sequence 103, Appl
8	Sequence 2, Appl
9	Sequence 2, Appl
10	Sequence 2, Appl
11	Sequence 2, Appl
12	Sequence 2, Appl
13	Sequence 2, Appl
14	Sequence 2, Appl
15	Sequence 2, Appl
16	Sequence 2, Appl
17	Sequence 2, Appl
18	Sequence 2, Appl
19	Sequence 2, Appl
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21	Sequence 2, Appl
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40	Sequence 2, Appl
41	Sequence 2, Appl
42	Sequence 2, Appl
43	Sequence 2, Appl
44	Sequence 2, Appl
45	Sequence 2, Appl

20	39	47.6	16	9	US-09-805-101-104	Sequence 104, Appl
21	38	46.3	13	9	US-09-805-101-7	Sequence 7, Appl
22	38	46.3	14	9	US-09-805-101-8	Sequence 8, Appl
23	38	46.3	14	10	US-09-805-101-9	Sequence 9, Appl
24	38	46.3	15	9	US-09-805-101-10	Sequence 10, Appl
25	36	43.9	13	9	US-09-805-101-101	Sequence 101, Appl
26	36	43.9	14	9	US-09-805-101-102	Sequence 102, Appl
27	36	43.9	15	9	US-09-805-101-103	Sequence 103, Appl
28	36	43.9	16	9	US-09-805-101-104	Sequence 104, Appl
29	36	43.9	16	10	US-09-805-101-105	Sequence 105, Appl
30	35	42.7	13	9	US-09-805-101-106	Sequence 106, Appl
31	35	42.7	13	9	US-09-805-101-107	Sequence 107, Appl
32	35	42.7	15	9	US-09-805-101-108	Sequence 108, Appl
33	35	42.7	15	10	US-09-805-101-109	Sequence 109, Appl
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35	34	41.5	10	9	US-09-805-101-111	Sequence 111, Appl
36	34	41.5	10	10	US-09-805-101-112	Sequence 112, Appl
37	34	41.5	11	9	US-09-805-101-113	Sequence 113, Appl
38	34	41.5	11	9	US-09-805-101-114	Sequence 114, Appl
39	34	41.5	12	9	US-09-805-101-115	Sequence 115, Appl
40	34	41.5	12	9	US-09-805-101-116	Sequence 116, Appl
41	34	41.5	12	9	US-09-805-101-117	Sequence 117, Appl
42	33	40.2	12	9	US-09-805-101-118	Sequence 118, Appl
43	33	40.2	14	10	US-09-805-101-119	Sequence 119, Appl
44	33	40.2	16	9	US-09-805-101-120	Sequence 120, Appl
45	33	40.2	16	9	US-09-805-101-121	Sequence 121, Appl

ALIGNMENTS

RESULT 1
US-08-910-386A-53
Sequence 53, Application US08910386A
Patent No. 6,441,041A1
GENE: INF-EMALIN
APPLICANT: Ronald, Pamela C.
APPLICANT: Wang, Guo-Liang
APPLICANT: Song, Wen-Yuang
APPLICANT: Hubert, Scot
APPLICANT: Richter, Todd
TITLE OF INVENTION: Procedures and Materials for Testing
TITLE OF INVENTION: Disease Resistance in Plants
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US08/910,386A
FILING DATE: 13-AUG-1997
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/COCKET NUMBER: 03100-00995000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear

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; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 13
; OTHER INFORMATION: /product= "OTHER"
; OTHER INFORMATION: /notes "Xaa = Ile, Met, Thr, Asn, Lys,
; OTHER INFORMATION: Ser or Ala"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 14
; OTHER INFORMATION: /product= "OTHER"
; OTHER INFORMATION: /notes "Xaa = Cys, Arg, Ser or Gly"
US-09-910-396A-53

Query Match 50.9% Score 41, DB 8, Length 14;
Best Local Similarity 72.7%, Pred No. 5.4,
Matches 8, Conservative 0, Mismatches 3, Indels 0, Gaps 0,

QY 3 PNYNYKPSK 13
|||||
Db 2 PNYNYKPYK 12

RESULT 2
US-09-805-301-45
; Sequence 45, Application US/0905301
; Patent No. US20020173456A1
; GENERAL INFORMATION:
; APPLICANT: Smith, Louis C.
; Sparrow, James T.
; Hauer, Jochen
; Mims, Martha P.
; TITLE OF INVENTION: LIPOPHILIC PEPTIDES FOR
; MACROMOLECULE DELIVERY
; NUMBER OF SEQUENCES: 139
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 433 West Fifth Street
; Suite 4700
; City: Los Angeles
; State: California
; Country: U S A
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM PC DOS 6.0
; SOFTWARE: Word Perfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/805,301
; FILING DATE: 12 Mar 2001
; CLASSIFICATION: Unknown
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 08/584,043
; FILING DATE: Unknown
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 017/189
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO. 45:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; OTHER INFORMATION: "Xaa" stands for any naturally
; occurring amino acid and
; analogues thereof.
; SEQUENCE DESCRIPTION: SEQ ID NO: 45:
US-09-910-396A-53

Query Match 47.8% Score 39, DB 9, Length 14;
Best Local Similarity 61.5%, Pred No. 10;
Matches 8, Conservative 0, Mismatches 5, Indels 0, Gaps 0;
; occurring amino acid and
; analogues thereof.
; SEQUENCE DESCRIPTION: SEQ ID NO: 45:
US-09-805-301-45

Query Match 47.8% Score 39, DB 9, Length 14;
Best Local Similarity 61.5%, Pred No. 10;
Matches 8, Conservative 0, Mismatches 5, Indels 0, Gaps 0;
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RESULT 7

US-09-806-301-103
Sequence 103, Application US/09/09/03/1
Patent No. US/09/09/03/103
GENERAL INFORMATION:
APPLICANT: Smith, Louis C.
Sparrow, James T.
Hauer, Jochen
Mims, Martha P.
TITLE OF INVENTION: LIPOPHILIC PEPTIDES FOR
MACROMOLECULE DELIVERY
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lynn S. Lynn
STREET: 633 West Fifth Street
Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2065
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
storage

COMPUTER IBM Corporation
OPERATING SYSTEM: DOS 6.0
SOFTWARE: Word Perfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/09/03/103
FILING DATE: 12 Mar 2003
CLASSIFICATION: C12N 251
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US/09/09/03/103
FILING DATE: UNKNOWN
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 42,427
REFERENCE/DOCKET NUMBER: 217/290
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-4510

INFORMATION FOR SEQ ID NO: 103:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 103:
US-09-806-301-103

Query March 47.63; Score 39; DB 9; Length 15;
Best Local Similarity 41.53; Pred. No. 11;
Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0

QY 4 KKKKKKKKKKKK 13
DB 1 KKKKKKKKKKKK 13

RESULT 8

US-09-806-301-103
Sequence 103, Application US/09/09/03/103
Patent No. US/09/09/03/103
GENERAL INFORMATION:
APPLICANT: Smith, Louis C.
Sparrow, James T.
Hauer, Jochen
Mims, Martha P.
TITLE OF INVENTION: LIPOPHILIC PEPTIDES FOR
MACROMOLECULE DELIVERY
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lynn S. Lynn
STREET: 633 West Fifth Street
Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2065
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
storage

COMPUTER IBM Corporation

CURRENT FILING DATE: 2001-02-16
PRICE APPLICATION NUMBER: 50/183,451
PRICE FILING DATE: 2000-02-18
NUMBER OF SEQ ID NOS: 21
SOFTWARE: PASTSEQ for Windows Version 4.0
SEQ ID NO: 2
LENGTH: 15
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: completely synthetic sequence
US-09-784-918-2

Query March 47.63; Score 39; DB 9; Length 15;
Best Local Similarity 40.08; Pred. No. 11;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0

QY 4 KKKKKKKKKKKK 13

DB 2 KKKKKKKKKKKK 11

RESULT 9

US-09-770-967-2
Sequence 2, Application US/09/07/06/7
Patent No. US/09/07/06/7
GENERAL INFORMATION:
APPLICANT: Verck & Co., Inc.
APPLICANT: Dinemate, Christopher J.
APPLICANT: Bergman, Jeffrey M.
TITLE OF INVENTION: Inhibitors of Prenyl Protein Transferase
FILE REFERENCE: 20495
PRIORITY APPLICATION NUMBER: US/09/07/06/7
CURRENT FILING DATE: 2001-02-16
PRICE APPLICATION NUMBER: 42/143,651
PRICE FILING DATE: 2000-02-18
NUMBER OF SEQ ID NOS: 21
SOFTWARE: PASTSEQ for Windows Version 4.0
SEQ ID NO: 2
LENGTH: 15
TYPE: PRT
ORGANISM: Homo sapien
US-09-770-967-2

Query March 47.63; Score 39; DB 10; Length 15;
Best Local Similarity 40.08; Pred. No. 11;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0

QY 4 KKKKKKKKKKKK 13

DB 2 KKKKKKKKKKKK 11

RESULT 10

US-09-806-301-103
Sequence 103, Application US/09/09/03/103
Patent No. US/09/09/03/103
GENERAL INFORMATION:
APPLICANT: Merck & Co., Inc.
APPLICANT: Williams, Theresa M.
APPLICANT: Stump, Craig A.
TITLE OF INVENTION: Inhibitors of Prenyl Protein Transferase
FILE REFERENCE: 20673
PRIORITY APPLICATION NUMBER: US/09/09/03/103
CURRENT FILING DATE: 2001-02-16
SOFTWARE: PASTSEQ for Windows Version 4.0
SEQ ID NO: 2
LENGTH: 15
TYPE: PRT
ORGANISM: Homo sapien

Query Match 47.6% Score 39; DB 10; Length 15;
Best Local Similarity 80.0%; Pred. No. 11;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 KKKKKKSPSV 13
| | | | | : |
DB 2 KKKKKKSPSV 11

RESULT 13
US-09-784-897A-2
; Sequence 2, Application US/8974897A
; Patent No. US20020052463A1
; GENERAL INFORMATION:
; APPLICANT: Merck & Co., Inc.
; APPLICANT: Dinsmore, Christopher J.
; APPLICANT: Bergman, Jeffrey M.
; TITLE OF INVENTION: FENIL PROTEIN TRANSFERASE INHIBITORS
; FILE REFERENCE: 20497
; CURRENT APPLICATION NUMBER: US/09/784,897A
; CURRENT FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: 96/193,449
; PRIOR FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: completely synthetic sequence
US-09-784-897A-2

Query Match 47.6% Score 39; DB 10; Length 15;
Best Local Similarity 80.0%; Pred. No. 11;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 KKKKKKSPSV 13
| | | | | : |
DB 2 KKKKKKSPSV 11

RESULT 14
US-09-770-983-2
; Sequence 2, Application US/09770983
; Patent No. US20020052380A1
; GENERAL INFORMATION:
; APPLICANT: Merck & Co., Inc.
; APPLICANT: Dinsmore, Christopher J.
; APPLICANT: Bergman, Jeffrey M.
; TITLE OF INVENTION: Inhibitors of Protein Protein Transferase
; FILE REFERENCE: 20309
; CURRENT APPLICATION NUMBER: US/09/770,983
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 96/193,450
; PRIOR FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homosapien
US-09-770-983-2

Query Match 47.6% Score 39; DB 10; Length 15;
Best Local Similarity 80.0%; Pred. No. 11;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 KKKKKKSPSV 13
| | | | | : |
DB 2 KKKKKKSPSV 11

RESULT 15
US-09-770-983-2
; Sequence 2, Application US/09770983
; Patent No. US20020052380A1
; GENERAL INFORMATION:
; APPLICANT: Merck & Co., Inc.
; APPLICANT: Dinsmore, Christopher J.
; APPLICANT: Bergman, Jeffrey M.
; TITLE OF INVENTION: Inhibitors of Protein Protein Transferase
; FILE REFERENCE: 20309
; CURRENT APPLICATION NUMBER: US/09/770,983
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 96/193,450
; PRIOR FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homosapien
US-09-770-983-2

Query Match 47.6% Score 39; DB 10; Length 15;
Best Local Similarity 80.0%; Pred. No. 11;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 KKKKKKSPSV 13
| | | | | : |
DB 2 KKKKKKSPSV 11

RESULT 16
US-09-770-983-2
; Sequence 2, Application US/09770983
; Patent No. US20020052380A1
; GENERAL INFORMATION:
; APPLICANT: Merck & Co., Inc.
; APPLICANT: Dinsmore, Christopher J.
; APPLICANT: Bergman, Jeffrey M.
; TITLE OF INVENTION: Inhibitors of Protein Protein Transferase
; FILE REFERENCE: 20309
; CURRENT APPLICATION NUMBER: US/09/770,983
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 96/193,450
; PRIOR FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homosapien
US-09-770-983-2

Query Match 47.6% Score 39; DB 10; Length 15;
Best Local Similarity 80.0%; Pred. No. 11;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 KKKKKKSPSV 13
| | | | | : |
DB 2 KKKKKKSPSV 11

RESULT 17
US-09-770-983-2
; Sequence 2, Application US/09770983
; Patent No. US20020052380A1
; GENERAL INFORMATION:
; APPLICANT: Merck & Co., Inc.
; APPLICANT: Dinsmore, Christopher J.
; APPLICANT: Bergman, Jeffrey M.
; TITLE OF INVENTION: Inhibitors of Protein Protein Transferase
; FILE REFERENCE: 20309
; CURRENT APPLICATION NUMBER: US/09/770,983
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 96/193,450
; PRIOR FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homosapien
US-09-770-983-2

Query Match 47.6% Score 39; DB 10; Length 15;
Best Local Similarity 80.0%; Pred. No. 11;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 KKKKKKSPSV 13
| | | | | : |
DB 2 KKKKKKSPSV 11

RESULT 18
US-09-770-983-2
; Sequence 2, Application US/09770983
; Patent No. US20020052380A1
; GENERAL INFORMATION:
; APPLICANT: Merck & Co., Inc.
; APPLICANT: Dinsmore, Christopher J.
; APPLICANT: Bergman, Jeffrey M.
; TITLE OF INVENTION: Inhibitors of Protein Protein Transferase
; FILE REFERENCE: 20309
; CURRENT APPLICATION NUMBER: US/09/770,983
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 96/193,450
; PRIOR FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homosapien
US-09-770-983-2

Query Match 47.6% Score 39; DB 10; Length 15;
Best Local Similarity 80.0%; Pred. No. 11;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 KKKKKKSPSV 13
| | | | | : |
DB 2 KKKKKKSPSV 11

RESULT 15

US-09-828-325A-3
Sequence 3, Application US/09929325A
Patent No. US20020068747A1
GENERAL INFORMATION:
APPLICANT: Merck & Co., Inc.
APPLICANT: Craig A. Stump
APPLICANT: Theresa M. Williams
TITLE OF INVENTION: INHIBITORS OF KENYL PROTEIN TRANSFERASE
FILE REFERENCE: 20636Y
CURRENT APPLICATION NUMBER: US/09/928,325A
CURRENT FILING DATE: 2001-08-17
PRIOR APPLICATION NUMBER: 60/136,244
PRIOR FILING DATE: 2000-04-10
NUMBER OF SEQ ID NOS: 25
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3
LENGTH: 15
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Completely Synthetic Amino Acid Sequence
US-09-828-325A-3

Query Match 47.6%; Score 39; EE 10; Length 15;
Best Local Similarity 80.0%; Pred. No. 11;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 KKKKKKSPSK 13
|||
Db 2 KKKKKKSKTK 11

Search completed: March 3, 2003, 06:55:21
Job time : 8 secs


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1 REGISTRATION NUMBER 30,207
2 REFERENCE/SECRET NUMBER 214/120
3 TELECOMMUNICATION INFORMATION
4 TELEPHONE: (213) 489-1600
5 TELEFAX: (213) 955-0440
6 TELEFAX: 67-2510
7 INFORMATION FOR SEQ ID NO: 46:
8 SEQUENCE CHARACTERISTICS:
9 LENGTH: 14 amino acids
10 TYPE: amino acid
11 STRANDEDNESS: single
12 TOPOLOGY: linear
13 MOLECULE TYPE: peptide
14 FEATURE:
15 OTHER INFORMATION: "Xaa" stands for any naturally
16 OTHER INFORMATION: occurring amino acid and
17 OTHER INFORMATION: analogues thereof
18 US 08 985 337A 46
19
20 Query Match 47 48: 80% 100 100 40: Length 14:
21 Best Local Similarity 61.5%, Pos: 1-18,
22 Matches 4: Conservative 0: Mismatches 5: Indels 0: Gaps 0:
23
24 QY 4 PPTPTPTPTPT 16
25 DB 2 PPTPTPTPTPT 14
26
27 RESULT 7
28 US-08-985-337A-1
29 Sequence 1, Application US/08-985337A
30 Patent No. 5932596
31 GENERAL INFORMATION:
32 APPLICANT: Ciccarone, Terrence M.
33 APPLICANT: Ciccarone, S. Jane
34 TITLE OF INVENTION: INHIBITORS OF FARNESYL PROTEIN
35 TITLE OF INVENTION: TRANSFERASE
36 NUMBER OF SEQUENCES: 14
37 CORRESPONDENCE ADDRESS:
38 ADDRESSEE: Merck & Co., Inc.
39 STREET: P.O. Box 2000, 126 E. Lincoln Ave.
40 CITY: Rahway
41 STATE: NJ
42 COUNTRY: USA
43 ZIP: 07065-0900
44 COMPUTER READABLE FORM:
45 MEDIUM TYPE: Diskette
46 COMPUTER: IBM Compatible
47 OPERATING SYSTEM: DOS
48 SOFTWARE: PASCAL for Windows Version 2.0
49 CURRENT APPLICATION DATA:
50 APPLICATION NUMBER: US/08/985,337A
51 FILING DATE:
52 CLASSIFICATION:
53 PRIOR APPLICATION DATA:
54 APPLICATION NUMBER: 60/347,572
55 FILING DATE: 25 DEC 1996
56 ATTORNEY/AGENT INFORMATION:
57 NAME: Mubhard, David A.
58 REGISTRATION NUMBER: 35,297
59 REFERENCE/SECRET NUMBER: 14834Y
60 TELECOMMUNICATION INFORMATION:
61 TELEPHONE: 908-594-3903
62 TELEFAX: 908-594-4720
63 TELEX:
64 INFORMATION FOR SEQ ID NO: 1
65 SEQUENCE CHARACTERISTICS:
66 LENGTH: 15 amino acids
67 TYPE: amino acid
68 STRANDEDNESS: single
69 TOPOLOGY: linear
70 MOLECULE TYPE: protein
71 US-08-985-337A-1
72
73 Query Match 47 48: 80% 100 100 40: Length 15:
74 Best Local Similarity 61.5%, Pos: 1-18,
75 Matches 4: Conservative 0: Mismatches 1: Indels 0: Gaps 0:
76
77 QY 4 PPTPTPTPTPT 13
78 DB 2 PPTPTPTPTPT 11
79
80 RESULT 9
81 US-08-985-320A-1
82 Sequence 1, Application US/08-985320A
83 Patent No. 5977134
84 GENERAL INFORMATION:
85 APPLICANT: Ciccarone, Terrence M.
86 APPLICANT: Ciccarone, S. Jane
87 APPLICANT: Balczonko, Wacyl
88 APPLICANT: Hutchinson, John H.
89 APPLICANT: Lumma, Jr., William C.
```



```

; APPLICANT: Huber, Hans E.
; APPLICANT: Embrey, Mark W.
; TITLE OF INVENTION: A METHOD OF TREATING CANCER
; FILE REFERENCE: 1997-047
; CURRENT APPLICATION NUMBER: US/01/149,557A
; CURRENT FILING DATE: 1998-08-26
; EARLIER APPLICATION NUMBER: 50/057,145
; EARLIER FILING DATE: 1997-08-27
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 13
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthesized peptide substrate for
; OTHER INFORMATION: geranylgeranyl protein transferase type 1
US-09-140-567-13
Query Match 47.6%; Score 39; DB 3; Length 15;
Best Local Similarity 90.0%; Pred. No. 7.2;
Matches 8; Conservative 1; Mismatches 1; Indels 1; Gaps 0;
CY 4 KKKKKSPSK 13
DB 2 KKKKKSKTK 11
|||||:|

RESULT 13
US-09-170-951-13
; Sequence 13, Application US/01/170,951
; Patent No. 6101721
; GENERAL INFORMATION:
; APPLICANT: Bergman, Jeffrey M.
; APPLICANT: Ginsburg, Christopher J.
; APPLICANT: Graham, Samuel L.
; APPLICANT: Merck & Co., Inc.
; TITLE OF INVENTION: INHIBITORS OF PARAOXYL PROTEIN
; FILE REFERENCE: 1997-077
; CURRENT APPLICATION NUMBER: US/01/170,951
; CURRENT FILING DATE: 1998-10-14
; EARLIER APPLICATION NUMBER: 50/054,142
; EARLIER FILING DATE: 1997-10-17
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 13
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homosapien
US-09-170-951-13
Query Match 47.6%; Score 39; DB 3; Length 15;
Best Local Similarity 90.0%; Pred. No. 7.2;
Matches 8; Conservative 1; Mismatches 1; Indels 1; Gaps 0;
CY 4 KKKKKSPSK 13
DB 2 KKKKKSKTK 11
|||||:|

RESULT 14
US-09-164-482-13
; Sequence 13, Application US/01/164,482A
; Patent No. 6127390
; GENERAL INFORMATION:
; APPLICANT: Merck & Co., Inc.
; APPLICANT: Desolms, S. Jane
; APPLICANT: Lumma, William C.
; APPLICANT: Shaw, Anthony W.
; APPLICANT: Sisko, John T.
; APPLICANT: Tucker, Thomas J.
; TITLE OF INVENTION: INHIBITORS OF PEROXYL PROTEIN TRANSFERASE
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; FILE REFERENCE: 1997-047
; CURRENT APPLICATION NUMBER: US/01/149,557A
; CURRENT FILING DATE: 1998-10-01
; EARLIER APPLICATION NUMBER: 50/057,145
; EARLIER FILING DATE: 1997-10-02
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 13
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthesized peptide substrate for
; OTHER INFORMATION: geranylgeranyl protein transferase type 1
US-09-164-482-13
Query Match 47.6%; Score 39; DB 3; Length 15;
Best Local Similarity 90.0%; Pred. No. 7.2;
Matches 8; Conservative 1; Mismatches 1; Indels 1; Gaps 0;
CY 4 KKKKKSPSK 13
DB 2 KKKKKSKTK 11
|||||:|

RESULT 15
US-09-332-769-2
; Sequence 2, Application US/01/332,769
; Patent No. 6172076
; GENERAL INFORMATION:
; APPLICANT: Embrey, Mark W.
; APPLICANT: Perlow, Debra S.
; APPLICANT: Wai, John S.
; APPLICANT: Hoffman, Jacob M.
; TITLE OF INVENTION: INHIBITORS OF PEROXYL PROTEIN
; FILE REFERENCE: 1992-027
; CURRENT APPLICATION NUMBER: US/01/332,769
; CURRENT FILING DATE: 1999-06-14
; EARLIER APPLICATION NUMBER: US 60/089,311
; EARLIER FILING DATE: 1998-06-15
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homosapien
US-09-332-769-2
Query Match 47.6%; Score 39; DB 4; Length 15;
Best Local Similarity 90.0%; Pred. No. 7.2;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
CY 4 KKKKKSPSK 13
DB 2 KKKKKSKTK 11
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Search completed: March 3, 2003, 06:47:02
Job time : 16.6667 secs
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GenCore version 3.1.1
Sat 1993 2003 09:00:00

using sw model

01. 07:02:00 / Search time 15 Seconds
(with all alignments)
81776 William cell updates/sec

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08772 14

01-41 0.5

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01-41 results predictability chance to have a
equal to the score of the results of the
years of the total score distribution.

SUMMARIES

MP	ID	Description
1	A42089	transcription factor 1 (TCF1), alternative splice form, fruit fly, Drosophila melanogaster
2	P00040	glycogen phosphorylase (EC 2.4.1.1), cardiac, pig (Sus scrofa domestica)
3	S33603	chaperone, ribosome
4	P00785	NADH dehydrogenase
5	S64573	hypothetical protein
6	S69402	NAD(+) glycohydrol
7	S14135	DNA-binding protein
8	S11380	leberin 1 isoform
9	A60494	antigen-plas-1 gly
10	S13444	alpha-1,4-galactosyl transferase
11	S58571	48kDa bile/galactosyl transferase
12	P00045	porin porin - Arabi
13	P01598	to H chain V-D-J r
14	P07070	unidentified 27.2k
15	P00040	head, shock domain
16	P00040	cell receptor to
17	P00040	thymic humoral fac
18	P00040	cell receptor be
19	P00040	spectrin alpha cha
20	P00040	inhibin beta-A cha
21	S10325	4-hydroxyphenyl ac
22	S10325	4-hydroxyphenyl ac
23	P00040	cell receptor be
24	S10325	proteasome chain 1
25	S10325	translation elonga
26	P00040	alcohol dehydrogen
27	S10325	lignin peroxidase
28	S10325	methyl group/mw
29	P00040	heavy chain CD

30	16	22.9	5	2	P00040	cell receptor be
31	16	22.9	6	2	P00040	cell receptor be
32	16	22.9	6	2	P00040	cell receptor be
33	16	22.9	7	2	P00040	cell receptor be
34	16	22.9	7	2	P00040	cell receptor be
35	16	22.9	10	2	S65187	myochrome c oxid
36	16	22.9	10	2	P00040	cell receptor be
37	16	22.9	12	2	S10325	transferrin A1
38	16	22.9	12	2	P00040	cell receptor be
39	16	22.9	13	2	P00040	cell receptor be
40	16	22.9	13	2	S64126	hypothetical prote
41	16	22.9	13	2	S54344	glycylaldehyde
42	16	22.9	14	2	H64008	hypothetical prote
43	16	22.9	14	2	A41589	25g elastin bindin
44	16	22.9	14	2	P00040	cell receptor be
45	16	22.9	14	2	P00040	cell receptor be

ALIGNMENTS

RESULT 1

A42089

transcription factor 1 (TCF1), alternative splice form, fruit fly, Drosophila melanogaster

C:Species: Drosophila melanogaster

C:Date: 04-Mar-1993 #sequence: revision 10-Nov-1994 #rev: change 20-Mar-1994

C:Accession: A42089

R:Tracy, M.N.; Neilson, L.I.; Turner, E.E.; He, X.; Rosenfeld, M.S.

Cell 68, 491-505, 1992

A:Title: Twin of 1 TCF, a two amino acid difference in the 17th amino acid main domain

A:Reference number: A42089; MIM:224565; PMID:134764

A:Accession: A42089

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-10 <TR>

A:Cross references: GR:582271; NID:3245317; PMID:245518

A:Note: sequence extracted from RCF 134764

A:Genetics:

A:Gene: FlyBase:lpou

A:Cross references: FlyBase:FlyBase:lpou04418

Query Match 38.6% Score 27; DB 2; Length 10

Best Local Similarity 50.0%; Pred. No. 1; Size 10

Matches 4; Conservative 4; Mismatches 0; Inbels 0; Gaps 0

QY 4 GYKPKYS 11

IB 1 GYKPKYS 8

RESULT 2

P00040

glycogen phosphorylase (EC 2.4.1.1), cardiac, pig (Sus scrofa domestica)

C:Species: Sus scrofa domestica

C:Date: 10-Jun-1993 #sequence: revision 10-Jun-1993 #rev: change 11-May-2000

C:Accession: P00040

R:Dombadi, V.; Willis, A.C.; Vereb, G.; Johnson, L.N.

Comp. Biochem. Physiol. B 91, 217-227, 1998

A:Title: The sequence around the phosphorylation site of the porcine heart type 1b phosphorylase

A:Reference number: P00040; MIM:224569

A:Accession: P00040

A:Molecule type: protein

A:Residues: 1-14 <DOM>

A:Experimental source: heart

C:Keywords: phosphorylation; cardiac muscle; glycogen; metabolic; phosphorylation

Phosphorylation site: phosphorylation; cardiac muscle; glycogen; metabolic; phosphorylation

Query Match 34.3% Score 24; DB 2; Length 14

Best Local Similarity 44.4%; Pred. No. 2; Size 14

Matches 4; Conservative 4; Mismatches 1; Inbels 0; Gaps 0

QY 2 GYKPKYS 11

IB 1 GYKPKYS 8

amputation polymerase chain reaction Viper lebetina venom: isolated
MW: 136354856; PMID: 11914

QY

Score 19; 18.0; Length 12;

Best Local Similarity 75.0%; Pred. No. 13; 04;
Matches 3; Mismatches 1; Indels 0; Gaps 0;

Query Match 25.7%; Score 18; DB 2; Length 14;
Best Local Similarity 75.0%; Pred. No. 13; 04;
Matches 3; Mismatches 1; Indels 0; Gaps 0;

Query Match 25.7%; Score 18; DB 2; Length 14;
Best Local Similarity 75.0%; Pred. No. 13; 04;
Matches 3; Mismatches 1; Indels 0; Gaps 0;

QY

Score 18; 18.0; Length 12;

Best Local Similarity 75.0%; Pred. No. 13; 04;
Matches 3; Mismatches 1; Indels 0; Gaps 0;

QY

Score 18; 18.0; Length 12;

Best Local Similarity 75.0%; Pred. No. 13; 04;
Matches 3; Mismatches 1; Indels 0; Gaps 0;

QY

Score 18; 18.0; Length 12;

Best Local Similarity 75.0%; Pred. No. 13; 04;
Matches 3; Mismatches 1; Indels 0; Gaps 0;

QY

Score 18; 18.0; Length 12;

Best Local Similarity 75.0%; Pred. No. 13; 04;
Matches 3; Mismatches 1; Indels 0; Gaps 0;

QY

Score 18; 18.0; Length 12;

Best Local Similarity 75.0%; Pred. No. 13; 04;
Matches 3; Mismatches 1; Indels 0; Gaps 0;

C:Accession: G58501
R:Binette, J.P.; Binette, M.B.
submitted to the Protein Sequence Database, October 1994
A:Description: The proteins of kidney and gallbladder stones.
A:Reference number: A58501
A:Accession: G58501
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-10 <BIN>
A:Experimental source: human bile and gallbladder stones
A:Note: 1-Ser and 4-Glu were also found

QY

Score 18; 18.0; Length 12;

Best Local Similarity 75.0%; Pred. No. 13; 04;
Matches 3; Mismatches 1; Indels 0; Gaps 0;

QY

Score 18; 18.0; Length 12;

Best Local Similarity 75.0%; Pred. No. 13; 04;
Matches 3; Mismatches 1; Indels 0; Gaps 0;

QY

Score 18; 18.0; Length 12;

Best Local Similarity 75.0%; Pred. No. 13; 04;
Matches 3; Mismatches 1; Indels 0; Gaps 0;

QY

Score 18; 18.0; Length 12;

Best Local Similarity 75.0%; Pred. No. 13; 04;
Matches 3; Mismatches 1; Indels 0; Gaps 0;

QY

Score 18; 18.0; Length 12;

Best Local Similarity 75.0%; Pred. No. 13; 04;
Matches 3; Mismatches 1; Indels 0; Gaps 0;

QY

Score 18; 18.0; Length 12;

Best Local Similarity 75.0%; Pred. No. 13; 04;
Matches 3; Mismatches 1; Indels 0; Gaps 0;

QY

Score 18; 18.0; Length 12;

Best Local Similarity 75.0%; Pred. No. 13; 04;
Matches 3; Mismatches 1; Indels 0; Gaps 0;

QY

Score 18; 18.0; Length 12;

Best Local Similarity 75.0%; Pred. No. 13; 04;
Matches 3; Mismatches 1; Indels 0; Gaps 0;

QY

Score 18; 18.0; Length 12;

Best Local Similarity 75.0%; Pred. No. 13; 04;
Matches 3; Mismatches 1; Indels 0; Gaps 0;

C:Species: Mus musculus (house mouse)
 C:Date: 18-Aug-2003 #seqrev=1 #rev=1 #rev_change=18 Aug 2000
 C:Accession: PC7079
 P:Tsugita, A.; Kawakami, T.; Uchida, T.; Sakai, T.; Kato, M.; Matsui, T.; Watanabe, Y.;
 Electrophoresis 21, 1853-1871, 2000
 A:Title: Proteome analysis of mouse brain: Two-dimensional electrophoresis profiles of
 A:Reference number: PC7072
 A:Accession: PC7079
 A:Molecule type: protein
 A:Residues: 1-14 <TSU>
 A:Experimental source: strain C57BL/6Jr Slc, male; brain; striatum
 C:Keywords: brain

Query Match 25.71, Score 18; DB 2; Length 14;
 Best Local Similarity 42.94; Pred. No. 1.3e+04;
 Matches 3; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 6 KKKKKK 12
 DB 7 KKEESE 13

RESULT 15

A37789
 heat shock cognate protein 70 rat (fragment)
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 30-Apr-1991 #seqrev=1 #rev=1 #rev_change=18 Jun 1993
 C:Accession: A37789
 R:Mandell, R.B.; Feldherr, C.M.
 J. Cell Biol. 111, 1775-1783, 1990
 A:Title: Identification of 15 kDa HSP70 related heat shock cognate proteins that are capable of
 A:Reference number: A37782, WJBP 1, 1132, PWT 123173
 A:Accession: A37789
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-14 <MAN>

Query Match 25.71, Score 18; DB 2; Length 14;
 Best Local Similarity 56.71; Pred. No. 1.3e+04;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 KKKKKK 10
 DB 9 KKKKKK 14

Search completed: March 3, 2003, 07:05:09
 Job time : 16 secs


```

SH BLOC OR RPS19.
SC Other information: phytoplasmataceae; Achleoplasmataceae;
OC Bacteria; Firmicutes; Mollicutes; Achleoplasmataceae;
OC Achleoplasmataceae; Phytoplasmataceae;
OC NCBI_TaxID=35773;
RN [1] _
RP SEQUENCE FROM N.A.
RX MEDLINE=9436002; PubMed=9071198;
RA Gunderson D.E., Lee I.M., Rehner S.A., Davis P.E., Kingsbury D.T.;
RT "Phylogeny of mycoplasma-like organisms (phytoplasmataceae) a basis for
RT their classification."
PL J. Bacteriol. 176:5244-5254(1994).
CC 1- FUNCTION: FERTILIN IS A MEMBER WITH THE THAT BINDS TO THE
CC TO THE 16S RIBOSOMAL RNA (BY SIMILARITY).
CC 1- SIMILARITY: BELONGS TO THE SIFP FAMILY OF RIBOSOMAL PROTEINS.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
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CC entities requires a license agreement (see http://www.ebi.ac.uk/submit/
CC or send an email to license@ebi.ac.uk).
CC
CC BMRB: L27011; AAA89392.1;
DR ICD:011; ICD:011; Eukaryota;
FE ICD:011; Eukaryota; RIBOSOMAL_SIFP; PARTIAL
KW Ribosomal protein; rRNA-binding.
FT NON_TER 1
SC SEQUENCE 14 AA, 1642 MW, 22247PDBEFEE4AP DRC64;

Query Match 35.7% Score 25; DB 1; Length 14;
Best Local Similarity 50.0%; Pred No. 3.7e+02; Indels 0; Gaps 0;
Matches 0; Conservations 2; Mismatches 0;

CY 1 AAGGKKNOKK 10
  |||
  AAGGKKNOKK 14

RESULT 3
RPS19 LOWER STANDARD; PRT; 14 AA.
ID R319 LOWER STANDARD; PRT; 14 AA.
AC C48678.
DT 30 MAY 2000 (rel. 39, Created)
DT 30 MAY 2000 (rel. 39, Last sequence update)
DE 30S ribosomal protein S19 (fragment)
DE RPS19 OR RPS19.
OS Eukaryota; Metazoa; Chordata; Vertebrata; Ascidiacea;
OC Bacteria; Firmicutes; Mollicutes; Achleoplasmataceae;
OC Achleoplasmataceae; Phytoplasmataceae;
OC NCBI_TaxID=35773;
PN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9436002; PubMed=9071198;
RA Gunderson D.E., Lee I.M., Rehner S.A., Davis P.E., Kingsbury D.T.;
RT "Phylogeny of mycoplasma-like organisms (phytoplasmataceae) a basis for
RT their classification."
PL J. Bacteriol. 176:5244-5254(1994).
CC 1- FUNCTION: FERTILIN IS A MEMBER WITH THE THAT BINDS TO THE
CC TO THE 16S RIBOSOMAL RNA (BY SIMILARITY).
CC 1- SIMILARITY: BELONGS TO THE SIFP FAMILY OF RIBOSOMAL PROTEINS.
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CC or send an email to license@ebi.ac.uk).
CC
CC BMRB: L27027; AAA89394.1;
DR ICD:011; ICD:011; Eukaryota;
FE ICD:011; Eukaryota; RIBOSOMAL_SIFP; PARTIAL
KW Ribosomal protein; rRNA-binding.
FT NON_TER 1
SC SEQUENCE 14 AA, 1642 MW, 22247PDBEFEE4AP DRC64;

Query Match 35.7% Score 25; DB 1; Length 14;
Best Local Similarity 50.0%; Pred No. 3.7e+02; Indels 0; Gaps 0;
Matches 0; Conservations 2; Mismatches 0;

CY 1 AAGGKKNOKK 10
  |||
  AAGGKKNOKK 14

RESULT 4
SPI HALBO STANDARD; PRT; 10 AA.
ID SPI HALBO STANDARD; PRT; 10 AA.
AC Q10597.
DT 01-OCT-1996 (rel. 34, Created)
DT 15-SEP-1996 (rel. 34, Last sequence update)
DE Serine protease inhibitor (fragment)
DE Serine protease inhibitor (fragment)
OS Halocynthia roretzi (Sea squirt)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Ascidiacea;
OC Bacteria; Firmicutes; Mollicutes; Achleoplasmataceae;
OC Achleoplasmataceae; Phytoplasmataceae;
OC NCBI_TaxID=35773;
PN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9630131; PubMed=8759295;
RA Shishikura E., Abe T., Ohtake S., Tanaka K.;
RT "Inhibition of the hemolymph of a solitary arthropod, Halocynthia
RT roretzi."
RT Comp. Biochem. Physiol. 114B:1-11(1996).
CC 1- FUNCTION: SERPINS INHIBITS TRYPSIN AND PLASMA KINETINASE ACTIVITY.
CC 1- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
DR InterPro: IPR000215; Serpin
DR PROSITE: PS00294; SERPIN; PARTIAL.
DE Serpin; Serine protease inhibitor; Glycophorin; Plasma.
FT NON_TER 10
SC SEQUENCE 10 AA, 1154 MW, 42250PDBEFEE4AP DRC64;

Query Match 34.3% Score 24; DB 1; Length 10;
Best Local Similarity 60.0%; Pred No. 3.9e+02; Indels 0; Gaps 0;
Matches 0; Conservations 2; Mismatches 0;

CY 0 PGGPKK 7
  |||
  PGGPKK 8

RESULT 5
RPS19 LOWER STANDARD; PRT; 12 AA.
ID R319 LOWER STANDARD; PRT; 12 AA.
AC C48678.
DT 30 MAY 2000 (rel. 39, Created)
DT 30 MAY 2000 (rel. 39, Last sequence update)
DE 30S ribosomal protein S19 (fragment)
DE RPS19 OR RPS19.
OS Eukaryota; Metazoa; Chordata; Vertebrata; Ascidiacea;
OC Bacteria; Firmicutes; Mollicutes; Achleoplasmataceae;
OC Achleoplasmataceae; Phytoplasmataceae;
OC NCBI_TaxID=35773;
PN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9436002; PubMed=9071198;
RA Gunderson D.E., Lee I.M., Rehner S.A., Davis P.E., Kingsbury D.T.;
RT "Phylogeny of mycoplasma-like organisms (phytoplasmataceae) a basis for
RT their classification."

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Update version 1.0.0
1993-2003. Copyright 1993.

mini sw model

1993-02-02-01, 01-01-01, 01-01-01
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at results predictability change to have a
equal to the score of the result being printed,
year of the total score distribution.

SUMMARY

CP	ID	Description
0	Q9303	Q9303 Chlamydia
1	Q84271	Q84271 human papillomavirus
2	Q8338	Q8338 oncofornychu
3	Q84271	Q84271 human papillomavirus
4	Q84271	Q84271 human papillomavirus
5	Q84271	Q84271 human papillomavirus
6	Q84271	Q84271 human papillomavirus
7	Q84271	Q84271 human papillomavirus
8	Q84271	Q84271 human papillomavirus
9	Q84271	Q84271 human papillomavirus
10	Q84271	Q84271 human papillomavirus
11	Q84271	Q84271 human papillomavirus
12	Q84271	Q84271 human papillomavirus
13	Q84271	Q84271 human papillomavirus
14	Q84271	Q84271 human papillomavirus
15	Q84271	Q84271 human papillomavirus
16	Q84271	Q84271 human papillomavirus
17	Q84271	Q84271 human papillomavirus
18	Q84271	Q84271 human papillomavirus
19	Q84271	Q84271 human papillomavirus
20	Q84271	Q84271 human papillomavirus
21	Q84271	Q84271 human papillomavirus
22	Q84271	Q84271 human papillomavirus
23	Q84271	Q84271 human papillomavirus
24	Q84271	Q84271 human papillomavirus
25	Q84271	Q84271 human papillomavirus
26	Q84271	Q84271 human papillomavirus
27	Q84271	Q84271 human papillomavirus
28	Q84271	Q84271 human papillomavirus
29	Q84271	Q84271 human papillomavirus
30	Q84271	Q84271 human papillomavirus
31	Q84271	Q84271 human papillomavirus
32	Q84271	Q84271 human papillomavirus
33	Q84271	Q84271 human papillomavirus
34	Q84271	Q84271 human papillomavirus
35	Q84271	Q84271 human papillomavirus
36	Q84271	Q84271 human papillomavirus
37	Q84271	Q84271 human papillomavirus
38	Q84271	Q84271 human papillomavirus
39	Q84271	Q84271 human papillomavirus
40	Q84271	Q84271 human papillomavirus
41	Q84271	Q84271 human papillomavirus
42	Q84271	Q84271 human papillomavirus
43	Q84271	Q84271 human papillomavirus
44	Q84271	Q84271 human papillomavirus
45	Q84271	Q84271 human papillomavirus

17	19	27.1	10	12	Q9303
18	19	27.1	10	12	Q9303
19	19	27.1	10	12	Q9303
20	19	27.1	10	12	Q9303
21	19	27.1	10	12	Q9303
22	19	27.1	10	12	Q9303
23	19	27.1	10	12	Q9303
24	19	27.1	10	12	Q9303
25	19	27.1	10	12	Q9303
26	19	27.1	10	12	Q9303
27	19	27.1	10	12	Q9303
28	19	27.1	10	12	Q9303
29	19	27.1	10	12	Q9303
30	19	27.1	10	12	Q9303
31	19	27.1	10	12	Q9303
32	19	27.1	10	12	Q9303
33	19	27.1	10	12	Q9303
34	19	27.1	10	12	Q9303
35	19	27.1	10	12	Q9303
36	19	27.1	10	12	Q9303
37	19	27.1	10	12	Q9303
38	19	27.1	10	12	Q9303
39	19	27.1	10	12	Q9303
40	19	27.1	10	12	Q9303
41	19	27.1	10	12	Q9303
42	19	27.1	10	12	Q9303
43	19	27.1	10	12	Q9303
44	19	27.1	10	12	Q9303
45	19	27.1	10	12	Q9303

ALIGNMENTS

RESULT 1

Q9303 PRELIMINARY; PPT; 14 AA.

AC Q9303, 01-MAY-2000 (TREMURel. 13, Created)

DT 01-MAY-2000 (TREMURel. 13, Last sequence update)

DT 01-JUN 2002 (TREMURel. 21, Last annotation update)

DE 27 kDa histone analog (Fragment).

OS Chlamydia trachomatis.

OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.

OX NCBI_TaxID=813;

RN [1]

RP SEQUENCE.

RX MEDLINE-92041597; PubMed:92041597;

RA Hackstadt T.;

RT "Purification and N-terminal amino acid sequences of Chlamydia trachomatis histone analogs";

RL J. Bacteriol. 173:7046-7049:1991.

PI NON-TER 14 14

SQ SEQUENCE 14 AA; 1519 MW; 4.35DA-AB49-9004; P004.

Query Match 40.0%; Score 28; DB 2; Length 14;

Best Local Similarity 50.0%; Pred. No. 7.2e+02;

Matches 5; Conservative 3; Microscopic 0; Indel 0; Gap 0;

QY 4 GYKFKKSKWT 13

Dh 3 GYKFKKSKWT 12

RESULT 2

Q84271 PRELIMINARY; PPT; 8 AA.

AC Q84271, 01-NOV-1996 (TREMURel. 01, Created)

DT 01-NOV-1996 (TREMURel. 01, Last sequence update)

DT 01-NOV 1998 (TREMURel. 09, Last annotation update)

DE Li protein (Fragment).

OS Human papillomavirus type 19.

J. Bacteriol.

EMBL: L27047; AAA83948.1; -

NON TER 1

SEQUENCE 14 AA; 1712 MW; 40C454E8F8F8F4A; 4E-64;

Query Match 31.4%; Score 22; DB 2; Length 14;

Best Local Similarity 62.5%; Pred. No. 5; Seq. 13;

Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Cv 2 KDKKKKK 9

Db 7 KDKKKKK 14

RESULT 9

Q93E20 PRELIMINARY; PRT; 9 AA;

AC Q93E20, 2001 (TIEMBLrel. 19, Created

DT 01-DEC-2001 (TIEMBLrel. 19, Last sequence update

DT 01-DEC-2001 (TIEMBLrel. 19, Last annotation update

DE SGPB (Fragment).

GN SGPB.

OS Streptococcus agalactiae

OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales

OC Streptococcaceae; Streptococcus

OX NCBI_TaxID=1311;

RN [1]

RF SEQUENCE FROM N.A.

RC STRAIN=090H;

EX MEDLINE=21424698; PubMed=11532154;

FA Franken C., Haase G., Brandt C., Weber-Heymann J., Martin S.,

FA Lammert C., Lodzinski A., Bulliken R., Speilberg R.,

RT "Horizontal gene transfer and host specificity of the *Streptococcus*RT *streptococcus*: the role of a putative composite transposon containingRT *scpB* and *lmb*."

RL Mol. Microbiol. 41:925-935(2001).

DR EMBL: AF327852; AAL10713.1; -

FT NON TER 1

SQ SEQUENCE 9 AA; 1146 MW; 5437A7A12A794; 8394;

Query Match 28.6%; Score 20; DB 2; Length 9;

Best Local Similarity 42.9%; Pred. No. 6; Seq. 6;

Matches 3; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Cv 6 KKKKKKK 12

Db 2 KKKKKKK 9

RESULT 10

Q25179 PRELIMINARY; PRT; 12 AA;

AC Q25179;

DT 01-JAN-1998 (TIEMBLrel. 05, Created

DT 01-JAN-1998 (TIEMBLrel. 05, Last sequence update

J. Bacteriol.

EMBL: L27047; AAA83948.1; -

NON TER 1

SEQUENCE 14 AA; 1712 MW; 40C454E8F8F8F4A; 4E-64;

Query Match 31.4%; Score 22; DB 2; Length 14;

Best Local Similarity 62.5%; Pred. No. 5; Seq. 13;

Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Cv 2 KDKKKKK 9

Db 7 KDKKKKK 14

RESULT 9

Q93E20 PRELIMINARY; PRT; 9 AA;

AC Q93E20, 2001 (TIEMBLrel. 19, Created

DT 01-DEC-2001 (TIEMBLrel. 19, Last sequence update

DT 01-DEC-2001 (TIEMBLrel. 19, Last annotation update

DE SGPB (Fragment).

GN SGPB.

OS Streptococcus agalactiae

OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales

OC Streptococcaceae; Streptococcus

OX NCBI_TaxID=1311;

RN [1]

RF SEQUENCE FROM N.A.

RC STRAIN=090H;

EX MEDLINE=21424698; PubMed=11532154;

FA Franken C., Haase G., Brandt C., Weber-Heymann J., Martin S.,

FA Lammert C., Lodzinski A., Bulliken R., Speilberg R.,

RT "Horizontal gene transfer and host specificity of the *Streptococcus*RT *streptococcus*: the role of a putative composite transposon containingRT *scpB* and *lmb*."

RL Mol. Microbiol. 41:925-935(2001).

DR EMBL: AF327852; AAL10713.1; -

FT NON TER 1

SQ SEQUENCE 9 AA; 1146 MW; 5437A7A12A794; 8394;

Query Match 28.6%; Score 20; DB 2; Length 9;

Best Local Similarity 42.9%; Pred. No. 6; Seq. 6;

Matches 3; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Cv 6 KKKKKKK 12

Db 2 KKKKKKK 9

RESULT 10

Q25179 PRELIMINARY; PRT; 12 AA;

AC Q25179;

DT 01-JAN-1998 (TIEMBLrel. 05, Created

DT 01-JAN-1998 (TIEMBLrel. 05, Last sequence update

RA Cotton M.D., Weidman J.M., Fujii C., Bowman C., Watthey L., Wallin E.,
 RA Hayer W.S., Borodovsky M., Rapp P.D., Smith H.O., Fraser C.M.,
 RA Venter J.C.,
 RT "The complete genome sequence of the gastric pathogen *Helicobacter*
 RT pylori".
 RL Nature 369 530-547(1997).
 DR EMBL: AE000559; AAD07512.1;
 DR TIGR: HP04297;
 FW Nucleotide sequence of the *Helicobacter pylori* genome
 SW SEQUENCE 10 AA, 1375 MW, 22050A94E132239 CRO64;

Query Match 28.6% Score 20, DP 16; Length 12;
 Best Local Similarity 42.9%, Pval 1e-04, Indels 0, Gaps 0,
 Matches 3, Conservative 4, Mismatches 4

QY 1 SKDGVK 7
 DB 2 NENGKE 8

RESULT 11

Q47693 PRELIMINARY; PRT; 13 AA.
 ID Q47693
 AC Q47693
 DT 01-NOV-1996 (TREMURel 01, Created)
 DT 01-MAY-2000 (TREMURel 13, Last sequence update)
 DT 01-MAY-2000 (TREMURel 13, Last annotation update)
 DE Elongation factor T8 (EF T8) (Fragment)
 GN TUFB.
 OS Escherichia coli.
 CC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Escherichia.
 CX NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE 83086657; PubMed 7412296.
 RA Hudson L., Rossi J., Landy A.,
 PT "Dual function transcripts specifying RNA and mRNA".
 RL Nature 324 422-423(1986).
 LR EMBL: X01857; J04777;
 KW Elongation factor, protein synthesis.
 FT NON TER 13
 SQ SEQUENCE 13 AA, 1017 MW, 04368EAA19E0B19 D5364;

Query Match 28.6% Score 20, DP 16; Length 12;
 Best Local Similarity 50.8%, Pval 1e-04, Indels 0, Gaps 0,
 Matches 4, Conservative 7, Mismatches 2

QY 7 YVFFGVY 14
 DB 3 KSVFFPY 10

RESULT 12

Q90ME9 PRELIMINARY; PRT; 13 AA.
 ID Q90ME9
 AC Q90ME9
 DT 01-MAY-2000 (TREMURel 13, Created)
 DT 01-MAY-2000 (TREMURel 13, Last sequence update)
 DT 01-MAY-2000 (TREMURel 13, Last annotation update)
 DE Elastin (Fragment).
 GN ELN.
 CC Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Eumetazoa; ml,
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea;
 CX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE 87274907; PubMed 30384507
 RA Indik J., Yeh K., Marlow S., Beall J., Beal Bloom J.,
 PA Beal Bloom J., Greenstein-Goldstein N.,
 PT "Nucleotide sequence of the 3' region of the human elastin gene, great at tandem
 RT of Alu repetitive sequences and few coding sequences".

Connect. Tissue Res. 16:197-211(1987).

RL [2]
 RN SEQUENCE FROM N.A.
 RP MEDLINE=000010; PubMed=097040;
 RA Zhang M.C., He L., Gira M., Yong S.B., Tiller G.E., Davidson J.M.,
 PT "Cutis laxa arising from frameshift mutations in exon 10 of the
 RT elastin gene (ELN)".
 RL Hum Biol Chem 274:941-946(1999).
 DR EMBL: U76476; AA:U783.1;
 FW NCI_TPP 1
 SW SEQUENCE 13 AA, 1348 MW, 43E1E1FBCAF8D03 F8C64;

Query Match 28.6% Score 20, DP 16; Length 12;
 Best Local Similarity 50.8%, Pval 1e-04, Indels 0, Gaps 0,
 Matches 3, Conservative 2, Mismatches 4

QY 4 GRKXK 8
 DB 9 GRKXK 13

RESULT 13

Q900X9 PRELIMINARY; PRT; 10 AA.
 ID Q900X9
 AC Q900X9
 DT 01-MAY-2000 (TREMURel 13, Created)
 DT 01-MAY-2000 (TREMURel 13, Last sequence update)
 DT 01-MAY-2000 (TREMURel 13, Last annotation update)
 DE Large T antigen (Fragment).
 GN Polyomavirus JC.
 CC Viruses; Icteria viruses; RNA viruses; Polyomaviridae.
 CX NCBI_TaxID=10332;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=0007644; PubMed=10616070;
 RA Bojelli-Mas S., Pina S., Giroues R.,
 PT "Detection of the JC virus in patients of polyomavirus in human
 RT epithelium by studying their presence in urban sewage".
 RL Appl Environ Microbiol 66:239-245(2000).
 DR EMBL: AF119145; AAF24004.1;
 FW NCI_TPP 1
 SW SEQUENCE 10 AA, 1000 MW, 47E6A0A0A0A0A0A0 F8C64;

Query Match 27.1% Score 10, DP 12; Length 10;
 Best Local Similarity 80.0%, Pval 1e-04;
 Matches 4, Conservative 0, Mismatches 1, Indels 0, Gaps 0

QY 9 KSKST 13
 DB 2 KSKPT 6

RESULT 14

Q900X7 PRELIMINARY; PRT; 10 AA.
 ID Q900X7
 AC Q900X7
 DT 01-MAY-2000 (TREMURel 13, Created)
 DT 01-MAY-2000 (TREMURel 13, Last sequence update)
 DT 01-MAY-2000 (TREMURel 13, Last annotation update)
 DE Large T antigen (Fragment).
 GN Polyomavirus JC.
 CC Viruses; Icteria viruses; RNA viruses; Polyomaviridae.
 CX NCBI_TaxID=10332;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN=BCN2;
 RX MEDLINE=0007544; PubMed=10616230;
 RA Bojelli-Mas S., Pina S., Giroues R.,
 PT "Detection of the JC virus in patients of polyomavirus in human
 RT epithelium by studying their presence in urban sewage".
 RL Appl Environ Microbiol 66:239-245(2000).
 DR EMBL: AF119145; AAF24004.1;

1. V01 4006A97771A-243-243
1.1.1. Score 13; IR 1.0; Length 10;
1.1.2. Pred. No. 1.0; 1.0;
1.1.3. Mismatches 0; Indels 0; Gaps 0;
1.1.4. PRT; : AA;
1.1.5. (1.0, treated);
1.1.6. Last sequence of 1.0;
1.1.7. Last annotation of 1.0;
1.1.8. No RNA stage; Polyomavirus;
1.1.9. 1.0; 1.0;
1.1.10. 1.0; 1.0;
1.1.11. 1.0; 1.0;
1.1.12. 1.0; 1.0;
1.1.13. 1.0; 1.0;
1.1.14. 1.0; 1.0;
1.1.15. 1.0; 1.0;
1.1.16. 1.0; 1.0;
1.1.17. 1.0; 1.0;
1.1.18. 1.0; 1.0;
1.1.19. 1.0; 1.0;
1.1.20. 1.0; 1.0;
1.1.21. 1.0; 1.0;
1.1.22. 1.0; 1.0;
1.1.23. 1.0; 1.0;
1.1.24. 1.0; 1.0;
1.1.25. 1.0; 1.0;
1.1.26. 1.0; 1.0;
1.1.27. 1.0; 1.0;
1.1.28. 1.0; 1.0;
1.1.29. 1.0; 1.0;
1.1.30. 1.0; 1.0;
1.1.31. 1.0; 1.0;
1.1.32. 1.0; 1.0;
1.1.33. 1.0; 1.0;
1.1.34. 1.0; 1.0;
1.1.35. 1.0; 1.0;
1.1.36. 1.0; 1.0;
1.1.37. 1.0; 1.0;
1.1.38. 1.0; 1.0;
1.1.39. 1.0; 1.0;
1.1.40. 1.0; 1.0;
1.1.41. 1.0; 1.0;
1.1.42. 1.0; 1.0;
1.1.43. 1.0; 1.0;
1.1.44. 1.0; 1.0;
1.1.45. 1.0; 1.0;
1.1.46. 1.0; 1.0;
1.1.47. 1.0; 1.0;
1.1.48. 1.0; 1.0;
1.1.49. 1.0; 1.0;
1.1.50. 1.0; 1.0;
1.1.51. 1.0; 1.0;
1.1.52. 1.0; 1.0;
1.1.53. 1.0; 1.0;
1.1.54. 1.0; 1.0;
1.1.55. 1.0; 1.0;
1.1.56. 1.0; 1.0;
1.1.57. 1.0; 1.0;
1.1.58. 1.0; 1.0;
1.1.59. 1.0; 1.0;
1.1.60. 1.0; 1.0;
1.1.61. 1.0; 1.0;
1.1.62. 1.0; 1.0;
1.1.63. 1.0; 1.0;
1.1.64. 1.0; 1.0;
1.1.65. 1.0; 1.0;
1.1.66. 1.0; 1.0;
1.1.67. 1.0; 1.0;
1.1.68. 1.0; 1.0;
1.1.69. 1.0; 1.0;
1.1.70. 1.0; 1.0;
1.1.71. 1.0; 1.0;
1.1.72. 1.0; 1.0;
1.1.73. 1.0; 1.0;
1.1.74. 1.0; 1.0;
1.1.75. 1.0; 1.0;
1.1.76. 1.0; 1.0;
1.1.77. 1.0; 1.0;
1.1.78. 1.0; 1.0;
1.1.79. 1.0; 1.0;
1.1.80. 1.0; 1.0;
1.1.81. 1.0; 1.0;
1.1.82. 1.0; 1.0;
1.1.83. 1.0; 1.0;
1.1.84. 1.0; 1.0;
1.1.85. 1.0; 1.0;
1.1.86. 1.0; 1.0;
1.1.87. 1.0; 1.0;
1.1.88. 1.0; 1.0;
1.1.89. 1.0; 1.0;
1.1.90. 1.0; 1.0;
1.1.91. 1.0; 1.0;
1.1.92. 1.0; 1.0;
1.1.93. 1.0; 1.0;
1.1.94. 1.0; 1.0;
1.1.95. 1.0; 1.0;
1.1.96. 1.0; 1.0;
1.1.97. 1.0; 1.0;
1.1.98. 1.0; 1.0;
1.1.99. 1.0; 1.0;
1.2. V01 4006A97771A-243-243
1.2.1. Score 13; IR 1.0; Length 10;
1.2.2. Pred. No. 1.0; 1.0;
1.2.3. Mismatches 0; Indels 0; Gaps 0;

1.1.1. 07:04:48



XX Claim 11; Page 70; 75pp; English

CC The present peptide sequence represents a specifically defined membrane binding element. The invention relates to a solid derivative (A) of a soluble polypeptide (B), which comprises at least 2 heavy residues

CC membrane-binding elements (MBE) of low membrane affinity covalently associated with (1) MRE interact, independently and with thermodynamic affinity, with components of cellular or artificial membranes exposed to extracellular fluids. (A) are used to treat disorders treatable with (1) itself, specifically inflammation or any other complement related disorder (e.g. neurological disease, graft rejection, myocardial infarction, sepsis, rheumatoid arthritis and many others), including application to indwelling devices and thrombolytic disease, but also treat allergy, intra weight loss, to treat ischaemia, to arrest and/or immunomodulate for treating multiple sclerosis (A) are administered orally, topically, by injection or inhalation at 0.01 to 10 mg/kg/day

XX Sequence 14 AA;

Query Match 100.00; Score 70; PP 14; Length 14;
Best Local Similarity 100.00; Prod. No. 00042;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SKDGRVWVWVSTV 14
DB 1 SKDGRVWVWVSTV 14
|||||

RESULT 2
ABR81241
ID ABR81241 standard; peptide; 14 AA.
AC ABR81241;
DT 20-NOV-2002 (first entry)
DE Antibacterial membrane binding peptide SEQ ID NO:4.
KW Antibacterial; glycopeptide; peptide; membrane associating element;
KW bacterial infection; vancomycin; rifampicin; polysynthetic inhibition;
KW antibiotic.
OS Synthetic.
XX WC20020612 A1.
XX 10-MAY-2002.
XX 02-NOV-2001; 2001W-GR04867
XX 01-NOV-2000; 2000P-0004924
XX (UYCA-) UNIV CAMBRIDGE TECH SERVICES LTD.
XX (ADPR-) ADPROTECH LTD.
XX Clasper MA, Botley CF,
XX WPI; 2002-4-1444/50
XX
PT Antibacterial compound, useful for the treatment of a bacterial
PT infection by 0.3 gram positive or negative bacteria, comprises a
PT conjugate of glycopeptide and peptidic membrane-associating element
XX
PS Claim 7; Page 57; 64pp; English.

CC The present invention describes an antibacterial compound and (1), comprising a conjugate of glycopeptide and peptidic membrane-associating element.
CC (1) describes the formula V, where V = a glycopeptide, which also
CC inhibits peptidoglycan biosynthesis in bacteria, i.e. a linking group,
CC is a peptidic membrane associating element, and X = H or a membrane
CC insertive element. Also described (2) a method of treating or preventing

CC a bacterial infection, comprising the administration of (1); and (2) use
CC of (1) in the manufacture of a medicament for the treatment or prevention
CC of a bacterial infection. (1) are used in the manufacture of a medicament
CC for the treatment or prophylaxis of a bacterial infection in a human or
CC animal body, including both the gastrointestinal and gram negative bacteria
CC including Mycobacterium sp., Enterobacter sp., Escherichia sp.,
CC Staphylococcus sp., Vibrio sp., Neisseria sp., Bacteria sp., Klebsiella
CC sp., Bacillus sp., Clostridium sp., Pseudomonas sp., Actinomyces sp.,
CC Rhodococcus sp., Gramella sp., particularly suitable for instant
CC bacterial strains. (1) are also useful as wound treatment agents to
CC prevent adhesion of bacteria to matrix proteins, especially fibrinectin,
CC exposed in wound tissue, and for prophylactic use in dental treatment as
CC an alternative to, or in combination with, antibiotic therapy. (1)
CC has stronger binding to bacterial membranes which have a higher
CC proportion of acidic phospholipids than the eubiotic organisms, also
CC having a higher proportion of membrane associated glycoprotein. (1)
CC vancomycin shows an enhanced activity against gram negative bacteria,
CC with (1) and is effective to treat the antibiotic resistant bacterial
CC strains. ABR81234 to ABR81272 represent peptides given in the
CC exemplification of the present invention.

XX Sequence 14 AA;

Query Match 100.00; Score 70; PP 23; Length 14;
Best Local Similarity 100.00; Prod. No. 00042;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SKDGRVWVWVSTV 14
DB 1 SKDGRVWVWVSTV 14
|||||

RESULT 3
AAV5859
ID AAV5859 standard; Peptide; 13 AA.
AC AAV5859,
XX 02-MAY-2000 (first entry)
XX Membrane binding element used in anti angiogenic polypeptide.
XX Anti-angiogenic; angiogenesis inhibitor; membrane binding element;
XX cancer; tumour; therapy.
XX Synthetic.
XX WO200004062-A2.
XX 27 JAN 2000.
XX 16-JUL-1999; 99W0-GR02792.
XX 16-JUL-1998; 98GB-0015505.
XX (ADPR-) ADPROTECH PLC.
XX Smith SAS, Bilgate CR, Steward M, Cox VR,
XX WPI; 2000-14,402/15.
XX
XX New soluble derivative of anti angiogenic polypeptide useful for
XX treatment of primary or secondary cancers, contains covalently attached
XX membrane-binding elements for targeting
XX
PS Claim 12; Page 32; 36pp; English.

CC The present sequence is a claimed example of a lysine-rich peptidic
CC membrane binding element, types that can be utilized to novel
CC soluble derivatives of anti angiogenic polypeptides of the
CC invention. (1) comprises a linking group, which is a linking group,
CC is a peptidic membrane associating element, and X = H or a membrane
CC insertive element. Also described (2) a method of treating or preventing

in macromolecules of DNA, RNA, molecule delivery;
the peptide; disease therapy; cell targeting.

antibiotics

any amino acid"

444

444

WHITING.

Chick Sparrow JTB

macromolecule conjugates used for the
delivery to cells, particularly for gene therapy

English.

A delivery peptide that can be used in the
context of the invention, the peptide-macromolecule
complex for delivery of a macromolecule into a cell.
The peptide-macromolecule complex comprising a
targetable lipophilic peptide (LP) comprising a
peptide with a lipid moiety, where the delivery
LP is complexed to the macromolecule. The
complex is used for the delivery of macromolecules such as nucleic
acids, lipids or carbohydrates. They can be
used for enhancing delivery of specific nucleic acids
into cells. They can also be used for gene
therapy. It is a transgenic animal for assessing human
peptides. They can also be used for livestock
breeding. The complex is capable of transporting the
macromolecule into the cell and releasing the molecule
into the cell. The complex can bind with a cell surface
protein and target the nucleus of the cell.

444 Score 42; ID 14; Length 14;

444; Pred. No. 5.0;

444; Mismatches 4; Labels 0; Gaps 0;

444 10 AA.

444

444; NGS; protein delivery;
penetrating peptide.

PD 07-MAR-2002.

XX 23 AUG 2001; 2001WJ 0266421.

XX 25 AUG 2001; 2001WJ 2276472.

PR 07-FEB-2001; 2001GR-0003110.

XX (AVET) AVENTIS PHARM INC.

XX Guo Y, Morse CC, Yao Z, Koosier GA;

XX WPI; 2003-094256/34.

XX New fusion proteins comprising membrane penetrating peptides, useful as

PT in vivo, ex vivo or in vitro intracellular carriers of delivery devices

PT for a compound of interest (e.g. peptide, protein, chemical entity,

PT nucleic acid)

XX Example 2, Page 27, 45pp, English.

XX This invention relates to a novel fusion protein, which comprises a

CC membrane penetrating peptide attached to a compound of interest.

CC The membrane penetrating peptide of the fusion protein is derived from a

CC nuclear localization signal and may be the nuclear localization signal

CC from human perleukin (HPEL). The fusion protein is useful for

CC delivery of a compound of interest into a cell. The fusion protein is

CC useful as in vivo, ex vivo or in vitro intracellular delivery devices

CC for a compound of interest (e.g. peptide, protein, chemical entity,

CC nucleic acid). In particular, the polypeptides are useful as protein

CC carriers for delivery of compounds to cells. The present invention

CC represents a new type of synthetic peptide used in an assay to analyze

CC the ability of different peptides to penetrate cellular membranes in

CC the examples of the invention.

XX Sequence 10 AA;

XX Query Match

XX Post-scan Similarity 98.98; Pred. No. 5.0;

XX Matches 9; Conservative 0; Mismatches 0; Gaps 0;

XX 4 0000000000 12

XX 1 0000000000 9

XX 1 0000000000 9

XX 1 0000000000 9

XX 1 0000000000 9

XX 1 0000000000 9

XX 1 0000000000 9

XX 1 0000000000 9

XX 1 0000000000 9

XX 1 0000000000 9

XX 1 0000000000 9

XX 1 0000000000 9

XX 1 0000000000 9

XX 1 0000000000 9

XX 1 0000000000 9

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XX 1 0000000000 9

XX 1 0000000000 9

XX 1 0000000000 9

XX 1 0000000000 9

XX 1 0000000000 9

XX 1 0000000000 9

XX 1 0000000000 9

XX 1 0000000000 9

XX 1 0000000000 9

XX 1 0000000000 9

XX WPI; Best result: 44
 XX Non naturally occurring gene therapy vector useful for gene therapy,
 PT comprising an inner shell having a core complex containing a nucleic
 PT acid and at least one complex forming reagent.
 XX Example 46; Page 99; 17pp; English
 XX The invention relates to a naturally occurring gene therapy vector,
 CC comprising an inner shell having a core complex containing a nucleic acid
 CC and at least one complex forming reagent. The vectors are stable during
 CC an improved outer shell layer that provides enhanced target specificity,
 CC in vivo and cell lysis ability. The vectors are relatively long-lived,
 CC and comprise thermally defined structures. The vectors demonstrate improved
 CC cell entry and intracellular trafficking, permitting enhanced nucleic
 CC acid therapeutic activity. Such is gene expression. The present sequence
 CC is that of the peptide P14, useful in the preparation of coated core
 CC complexes for the invention.
 XX
 XX Sequence 14 AA;
 XX
 XX Query Match: 59.03, Score 41, DB 00, Length 14;
 XX Best local similarity: 59.03, Field No. 8;
 XX Matches: 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 XX
 XX QY ? KKKKKKKKKKKKK 14
 XX | | | | | | | | | |
 XX DQ 1 KKKKKKKKKKKKK 13
 XX
 XX RESULT 11
 XX AAW38821
 XX ID AAW38821 standard; peptide; 10 AA.
 XX AC AAW38821;
 XX DT 30-MAR-1998 (first entry)
 XX DE Delivery peptide used in peptide-macromolecule complex
 XX
 XX Delivery peptide, peptide-macromolecule complex, gene molecule delivery,
 XX non-exchangeable lipophilic peptide, disease therapy; cell targeting.
 XX Synthetic.
 XX
 XX Key: Location/Qualifiers
 XX Misc-difference 9 /note "any amino acid"
 XX
 XX WO9725070-A2.
 XX 17-JUL-1997.
 XX 00-JAN-1997; 9AWO-US00454
 XX 08-JAN-1996; 9AUS-0584043.
 XX (BAYU) BAYLOR COLLEGE MEDICINE.
 XX Hauer J, Mims MP, Smith LC, Sparrow JT;
 XX WPI, 1997 372622/34.
 XX New lipophilic peptide-macromolecule complexes used for the
 XX delivery of macromolecules to cells, particularly for gene therapy
 XX
 XX Claim 6; Page 63; 106pp; English
 XX
 XX This sequence represents a delivery peptide that can be used in the
 XX peptide-macromolecule complex of the invention. The peptide-macromolecule
 XX complex of the invention is for delivering a macromolecule into a cell,
 XX and comprises a non-exchangeable lipophilic peptide. The peptide-macromolecule
 XX delivery peptide associated with a lipid moiety, where the delivery
 XX peptide portion of the peptide is complexed to the macromolecule. The
 XX complexes can be used for the delivery of macromolecules such as nucleic
 XX acids, proteins, and nucleic acids, lipids, and antibodies. They can be
 XX used to treat diseases by enhancing delivery of specific nucleic acids
 XX the appropriate targeted cells. They can also be used to create
 XX transgenic cells as well as transgenic animals for assessing human

XX delivery peptide associated with a lipid moiety, where the delivery
 XX peptide portion of the peptide is complexed to the macromolecule. The
 XX complexes can be used for the delivery of macromolecules such as nucleic
 XX acids, proteins, and nucleic acids, lipids, and antibodies. They can be
 XX used to treat diseases by enhancing delivery of specific nucleic acids
 XX the appropriate targeted cells. They can also be used to create
 XX transgenic cells as well as transgenic animals for assessing human
 XX
 XX Query Match: 57.11, Score 40, DB 16, Length 10;
 XX Best local similarity: 57.11, Field No. 8.3;
 XX Matches: 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 XX
 XX QY S KKKKKKKKKKK 14
 XX | | | | | | | | | |
 XX DQ 1 KKKKKKKKKKK 10
 XX
 XX RESULT 12
 XX AAW38922
 XX ID AAW38922 standard; peptide; 11 AA.
 XX AC AAW38922;
 XX DT 30-MAR-1998 (first entry)
 XX DE Delivery peptide used in peptide-macromolecule complex
 XX
 XX Delivery peptide, peptide-macromolecule complex, gene molecule delivery,
 XX non-exchangeable lipophilic peptide, disease therapy; cell targeting.
 XX Synthetic.
 XX
 XX Key: Location/Qualifiers
 XX Misc-difference 10 /note "any amino acid"
 XX
 XX WO9725070-A2.
 XX 17-JUL-1997.
 XX 02-JAN-1997; 9AWO-US00454.
 XX 08-JAN-1996; 9AUS-0584043.
 XX (BAYU) BAYLOR COLLEGE MEDICINE.
 XX Hauer J, Mims MP, Smith LC, Sparrow JT;
 XX WPI, 1997 372622/34.
 XX New lipophilic peptide-macromolecule complexes used for the
 XX delivery of macromolecules to cells, particularly for gene therapy
 XX
 XX Claim 6; Page 63; 106pp; English.
 XX
 XX This sequence represents a delivery peptide that can be used in the
 XX peptide-macromolecule complex of the invention. The peptide-macromolecule
 XX complex of the invention is for delivering a macromolecule into a cell,
 XX and comprises a non-exchangeable lipophilic peptide. The peptide-macromolecule
 XX delivery peptide associated with a lipid moiety, where the delivery
 XX peptide portion of the peptide is complexed to the macromolecule. The
 XX complexes can be used for the delivery of macromolecules such as nucleic
 XX acids, proteins, and nucleic acids, lipids, and antibodies. They can be
 XX used to treat diseases by enhancing delivery of specific nucleic acids
 XX the appropriate targeted cells. They can also be used to create
 XX transgenic cells as well as transgenic animals for assessing human

bel. They can also be used for livestock
The complex is capable of transporting the
in and condensed state and releasing the molecule
for. The complex can bind with a cell surface
and target the nucleus of the cell.

14: Score 40; PP 16; Ident 11;
24: Pred. No. 9;
Matches 5; Mismatches 0; Indels 0; Gaps 0;

14: 12 AA.

17

peptide macromolecule.

pe-macromolecule complex for molecule delivery;
the peptide; disease therapy; cell targeting.

n/Qualifiers

"any amino acid"

484.

1943.

VENTURE.

4: 10, Sparrow CT.

a molecule and amino acid for the
cells, particularly for gene therapy
English.

a delivery peptide can be used in the
plex of the invention. The peptide-macromolecule
is for delivering a molecule into a cell.
carboxylate lipophilic peptide (LP) comprising a
del with a lipid moiety, where the delivery
LP is complexed to the cell molecule. The
or the delivery of macromolecules such as nucleic
acids, lipids or carbohydrates. They can be
ly enhancing delivery of nucleic acids into
cells. They can also be used to create
as transgenic animals for assessing human
del. They can also be used for livestock
the complex is capable of transporting the
le and condensed state and releasing the molecule
for. The complex can bind with a cell surface
and target the nucleus of the cell.

Query Match 57.1%; Score 40; PP 16; Ident 11;
Best Local Similarity 59.24; Pred. No. 9;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 YYYVYYVYVY 14
|||||
DR 3 YYYVYYVYVY 12

RESULT 14

AAW38867
ID AAW38867 standard; peptide; 13 AA.

XX AC AAW38867;

XX DT 30-MAR-1998 (first entry)

XX DE Delivery peptide used in peptide macromolecule complex.

XX FW Delivery peptide, peptide-macromolecule complex for molecule delivery;
non-exchangeable lipophilic peptide; disease therapy; cell targeting.

XX OS Synthetic.

XX EN WC9725376-A2.

XX PD 17-JUL-1997.

XX PF 02-JAN-1997; 97WO-US00454.

XX PR 09-JAN-1996; 96US-0584043.

XX PA (BAYU) BAYLOR COLLEGE MEDICINE.

XX PI Hauer J, Mims MP, Smith LC, Sparrow CT;

XX DR WPI; 1997 372622/34.

XX PT New lipophilic peptide macromolecule complexes used for the
delivery of macromolecules to cells, particularly for gene therapy

XX PS Disclosure; Page 51; 106pp; English.

XX CC This sequence represents a delivery peptide that can be used in the
peptide-macromolecule complex of the invention. The peptide-macromolecule
complex of the invention is for delivering a macromolecule into a cell,
and comprises a non-exchangeable lipophilic peptide (LP) comprising a
delivery peptide associated with a lipid moiety, where the delivery
peptide portion of the LP is complexed to the macromolecule. The
complexes can be used for the delivery of nucleic acids, lipids or
acids, proteins, oligonucleotides, lipids or carbohydrates. They can be
used to treat diseases by enhancing delivery of specific nucleic acids
the appropriate targeted cells. They can also be used to create
transgenic animals for assessing human
disease in an animal model. They can also be used for livestock
genetic trait purposes. The complex is capable of transporting the
macromolecule in a stable and condensed state and releasing the molecule
into the cellular interior. The complex can bind with a cell surface
receptor, type an endosome and target the nucleus of the cell.

XX SQ Sequence 13 AA;

Query Match 57.1%; Score 40; PP 16; Ident 11;
Best Local Similarity 59.24; Pred. No. 9;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YDGVVYYVYVY 14
|||||
DR 1 YDGVVYYVYVY 13

RESULT 15

AAW38787
 ID AAW38787 standard; peptide; 13 AA.
 AC AAW38787;
 XX
 DT 30-MAR-1998 (first entry)
 XX
 DE Delivery peptide used in peptide macromolecule complex.
 XX
 KW Delivery peptide; peptide-macromolecule complex; macromolecule delivery;
 KW non-exchangeable lipophilic peptide; disease therapy; cell targeting.
 XX
 OS Synthetic.
 XX
 PN WCG725070-A2
 XX
 PD 17-JUL-1997.
 XX
 PF 02-JAN-1997, 97WC-0500454.
 XX
 PR 04-JAN-1996; 96US-0584043.
 XX
 PA (BAYU) BAYLOR COLLEGE MEDICINE.
 XX
 PI Hauer J, Mims MP, Smith LC, Sparrow JT;
 XX
 DP WPI; 1997 372622/34.
 XX
 PT New lipophilic peptide-macromolecule complexes - used for the
 PT delivery of macromolecules to cells, particularly for gene therapy
 XX
 PS Claim 6; Page 83; 106pp; English.
 XX
 CC This sequence represents a delivery peptide that can be used in the
 CC peptide-macromolecule complex of the invention. The peptide-macromolecule
 CC complex of the invention is for delivering a macromolecule into a cell,
 CC and comprises a non-exchangeable lipophilic peptide (LP) comprising a
 CC delivery peptide associated with a lipid moiety, where the delivery
 CC peptide portion of the LP is complexed to the macromolecule. The
 CC complexes can be used for the delivery of macromolecules such as nucleic
 CC acids, proteins, oligonucleotides, lipids or carbohydrates. They can be
 CC used to treat diseases by enhancing delivery of specific nucleic acid to
 CC the appropriate targeted cells. They can also be used to create
 CC transformed cells as well as transgenic animals for assessing human
 CC disease in an animal model. They can also be used for livestock
 CC agricultural purposes. The complex is capable of transporting the
 CC macromolecule in a stable and condensed state and releasing the molecule
 CC into the cellular interior. The complex can bind with a cell surface
 CC receptor, lyse an endosome and target the nucleus of the cell.
 XX
 SQ Sequence 13 AA;

Query Match 57.1%; Score 40; DB 18; Length 13;
 Best Local Similarity 60.2%, Ref. No. 11;
 Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 KKKKKKKKKKKK 14
 | | | | | | | | | |
 DQ 1 KKKKKKKKKKKK 13

Search completed March 3, 2003, 07:02:52
 Job time : 35 secs


```

SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULAR TYPE: peptide
FEATURE:
OTHER INFORMATION: "Xaa" stands for any naturally
occurring amino acid and
analogues thereof.
SEQUENCE DESCRIPTION: SEQ ID NO: 45
US-09-805-301-45

Query Match
Best Local Similarity 69.01; Score 42; DB 9; Length 13;
Matches 9; Conservative 0; Mismatches 4; Indels 0
CY 1 FFFFFFFFFF 14
DB 1 FFFFFFFFFF 13

RESULT 2
US-09-805-301-46
SEQUENCE 46, Affiliation: US060201745A1
Patent No. US060201745A1
GENERAL INFORMATION:
APPLICANT: Smith, Louis C.
Sparrow, James T.
Hauer, Jochen
Mims, Martha P.
TITLE OF INVENTION: LIPOPHILIC PEPTIDES FOR
MACROMOLECULE DELIVERY
NUMBER OF SEQUENCES: 139
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 6.0
SOFTWARE: Word Perfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/06/406,401
FILING DATE: 12-Mar-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/584,043
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/POCKET NUMBER: 217/189
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 955-0440
TELEFAX: (213) 955-0440
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULAR TYPE: peptide
FEATURE:
OTHER INFORMATION: "Xaa" stands for any naturally
occurring amino acid and
analogues thereof.
SEQUENCE DESCRIPTION: SEQ ID NO: 46
US-09-805-301-46

Query Match
Best Local Similarity 80.04; Score 40; DB 9; Length 14;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0
CY 5 FFFFFFFFFF 14

SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULAR TYPE: peptide
FEATURE:
OTHER INFORMATION: "Xaa" stands for any naturally
occurring amino acid and
analogues thereof.
SEQUENCE DESCRIPTION: SEQ ID NO: 42
US-09-805-301-42

Query Match
Best Local Similarity 69.01; Score 40; DB 9; Length 14;
Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0
CY 2 FFFFFFFFFF 14
DB 2 FFFFFFFFFF 14

RESULT 3
US-09-805-301-42
SEQUENCE 42, Affiliation: US060201745A1
Patent No. US060201745A1
GENERAL INFORMATION:
APPLICANT: Smith, Louis C.
Sparrow, James T.
Hauer, Jochen
Mims, Martha P.
TITLE OF INVENTION: LIPOPHILIC PEPTIDES FOR
MACROMOLECULE DELIVERY
NUMBER OF SEQUENCES: 139
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 6.0
SOFTWARE: Word Perfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/06/406,401
FILING DATE: 12-Mar-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/584,043
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/POCKET NUMBER: 217/189
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 955-0440
TELEFAX: (213) 955-0440
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
OTHER INFORMATION: "Xaa" stands for any naturally
occurring amino acid and
analogues thereof.
SEQUENCE DESCRIPTION: SEQ ID NO: 42
US-09-805-301-42

Query Match
Best Local Similarity 80.04; Score 40; DB 9; Length 14;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0
CY 5 FFFFFFFFFF 14
```



```

1 STREET: 633 West Fifth Street
2 SUITE: 4700
3 CITY: Los Angeles
4 STATE: California
5 COUNTRY: U.S.A.
6 ZIP: 90071-2066
7 COMPUTER READABLE FORM:
8 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
9
10 COMPUTER: IBM Compatible
11 OPERATING SYSTEM: IBM PC DOS 6.0
12 SOFTWARE: Word Perfect 6.1
13 CURRENT APPLICATION DATA:
14 APPLICATION NUMBER: US/09/805,301
15 FILING DATE: 12-Mar-2001
16 CLASSIFICATION: <Unknown>
17 PRIOR APPLICATION DATA:
18 APPLICATION NUMBER: 09/854,043
19 FILING DATE: <Unknown>
20 ATTORNEY/AGENT INFORMATION:
21 NAME: Warburg, Richard J.
22 REGISTRATION NUMBER: 32,127
23 REFERENCE/DOCKET NUMBER: 217/189
24 TELECOMMUNICATION INFORMATION:
25 TELEPHONE: (213) 489-1600
26 TELEFAX: (213) 955-0440
27 TELEX: 67-2510
28 INFORMATION FOR SEQ ID NO: 7:
29 SEQUENCE CHARACTERISTICS:
30 LENGTH: 13 amino acids
31 TYPE: amino acid
32 STRANDEDNESS: single
33 TOPOLOGY: linear
34 MOLECULE TYPE: peptide
35 SEQUENCE DESCRIPTION: SEQ ID NO: 7:
36 US-09-805-301-7
37
38 Query Match 57 18; Score 40; ID 9; Length 13;
39 Best Local Similarity 69.23; Prod No 4.6;
40 Matches 9; Conservation 9; Mismatches 4; Indels 0; Gaps 0;
41
42 QY 2 PGGVYVYVYVYVY 14
43 1 |||||
44 1 PGGVYVYVYVYVY 13
45
46 RESULT 7
47 US-09-805-301-101
48 Sequence 101, Application US/09/805,301
49 Patent No US20020173456A1
50 GENERAL INFORMATION:
51 APPLICANT: Smith, Louis C.
52 Sparrow, James T.
53 Hauer, Jochen
54 Mims, Martha P.
55 TITLE OF INVENTION: LIPOPHILIC PEPTIDES FOR
56 MACROMOLECULE DELIVERY
57 NUMBER OF SEQUENCES: 139
58 REFERENCE ADDRESS:
59 ADDRESSEE: Lyon & Lyon
60 STREET: 633 West Fifth Street
61 SUITE: 4700
62 CITY: Los Angeles
63 STATE: California
64 COUNTRY: U.S.A.
65 ZIP: 90071-2066
66 COMPUTER READABLE FORM:
67 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
68
69 COMPUTER: IBM Compatible
70 OPERATING SYSTEM: IBM PC DOS 6.0
71 SOFTWARE: Word Perfect 6.1
72 CURRENT APPLICATION DATA:
73 APPLICATION NUMBER: US/09/805,301
74 FILING DATE: 12-Mar-2001
75 CLASSIFICATION: <Unknown>
76 PRIOR APPLICATION DATA:
77 APPLICATION NUMBER: 09/854,043
78 FILING DATE: <Unknown>
79 ATTORNEY/AGENT INFORMATION:
80 NAME: Warburg, Richard J.
81 REGISTRATION NUMBER: 32,127
82 REFERENCE/DOCKET NUMBER: 217/189
83 TELECOMMUNICATION INFORMATION:
84 TELEPHONE: (213) 489-1600
85 TELEFAX: (213) 955-0440
86
87 RESULT 8
88 US-09-805-301-8
89 Sequence 8, Application US/09/805,301
90 Patent No US20020173456A1
91 GENERAL INFORMATION:
92 APPLICANT: Smith, Louis C.
93 Sparrow, James T.
94 Hauer, Jochen
95 Mims, Martha P.
96 TITLE OF INVENTION: LIPOPHILIC PEPTIDES FOR
97 MACROMOLECULE DELIVERY
98 NUMBER OF SEQUENCES: 139
99 REFERENCE ADDRESS:
100 ADDRESSEE: Lyon & Lyon
101 STREET: 633 West Fifth Street
102 SUITE: 4700
103 CITY: Los Angeles
104 STATE: California
105 COUNTRY: U.S.A.
106 ZIP: 90071-2066
107 COMPUTER READABLE FORM:
108 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
109
110 COMPUTER: IBM Compatible
111 OPERATING SYSTEM: IBM PC DOS 6.0
112 SOFTWARE: Word Perfect 6.1
113 CURRENT APPLICATION DATA:
114 APPLICATION NUMBER: US/09/805,301
115 FILING DATE: 12-Mar-2001
116 CLASSIFICATION: <Unknown>
117 PRIOR APPLICATION DATA:
118 APPLICATION NUMBER: 09/854,043
119 FILING DATE: <Unknown>
120 ATTORNEY/AGENT INFORMATION:
121 NAME: Warburg, Richard J.
122 REGISTRATION NUMBER: 32,127
123 REFERENCE/DOCKET NUMBER: 217/189
124 TELECOMMUNICATION INFORMATION:
125 TELEPHONE: (213) 489-1600
126 TELEFAX: (213) 955-0440

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US-09-214-913-41

US-09-214-913-41

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US-09-214-913-41

US-09-214-913-41

US-09-214-913-41

US-09-214-913-41

BT NUMBER: 217/189
SEQUENCE: 54.38; Score 18; DB 9; Length 11
Best Local Similarity 80.08; Pred. No. 619;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0

QV 5 KKKKKKKKK 14
DB 1 KKKKKKKKK 10

US-09-805-301-5
US-09-805-301-5
Sequence 5, Application US/0905301
Patent No. US20020173456A1
GENERAL INFORMATION:
APPLICANT: Smith, Louis C.
Sparrow, James T.
Hauer, Jochen
Mills, Martha P.
TITLE OF INVENTION: LIPOPHILIC PEPTIDES FOR
MACROMOLECULE DELIVERY
NUMBER OF SEQUENCES: 139
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 6.0
SOFTWARE: Word Perfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/0905301
FILING DATE: 12-Mar-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/584,043
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Waiburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/POCKET NUMBER: 217/189
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 6133510
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-805-301-5

Query Match
Best Local Similarity 80.08; Score 18; DB 9; Length 11
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0

QV 5 KKKKKKKKK 14
DB 1 KKKKKKKKK 10

US-09-805-301-5
US-09-805-301-5
Sequence 5, Application US/0905301
Patent No. US20020173456A1
GENERAL INFORMATION:
APPLICANT: Smith, Louis C.
Sparrow, James T.
Hauer, Jochen
Mills, Martha P.
TITLE OF INVENTION: LIPOPHILIC PEPTIDES FOR
MACROMOLECULE DELIVERY
NUMBER OF SEQUENCES: 139
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 6.0
SOFTWARE: Word Perfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/0905301
FILING DATE: 12-Mar-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/584,043
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Waiburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/POCKET NUMBER: 217/189
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 6133510
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-805-301-5

Query Match
Best Local Similarity 80.08; Score 18; DB 9; Length 11
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0

QV 5 KKKKKKKKK 14
DB 1 KKKKKKKKK 10

US-09-805-301-5
US-09-805-301-5
Sequence 5, Application US/0905301
Patent No. US20020173456A1
GENERAL INFORMATION:
APPLICANT: Smith, Louis C.
Sparrow, James T.
Hauer, Jochen
Mills, Martha P.
TITLE OF INVENTION: LIPOPHILIC PEPTIDES FOR
MACROMOLECULE DELIVERY
NUMBER OF SEQUENCES: 139
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 6.0
SOFTWARE: Word Perfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/0905301
FILING DATE: 12-Mar-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/584,043
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Waiburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/POCKET NUMBER: 217/189
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 6133510
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-805-301-5

Query Match
Best Local Similarity 80.08; Score 18; DB 9; Length 11
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0

QV 5 KKKKKKKKK 14
DB 1 KKKKKKKKK 10

US-09-805-301-5
US-09-805-301-5
Sequence 5, Application US/0905301
Patent No. US20020173456A1
GENERAL INFORMATION:
APPLICANT: Smith, Louis C.
Sparrow, James T.
Hauer, Jochen
Mills, Martha P.
TITLE OF INVENTION: LIPOPHILIC PEPTIDES FOR
MACROMOLECULE DELIVERY
NUMBER OF SEQUENCES: 139
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 6.0
SOFTWARE: Word Perfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/0905301
FILING DATE: 12-Mar-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/584,043
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Waiburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/POCKET NUMBER: 217/189
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 6133510
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-805-301-5

Query Match
Best Local Similarity 80.08; Score 18; DB 9; Length 11
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0

QV 5 KKKKKKKKK 14
DB 1 KKKKKKKKK 10

Search completed: March 3, 2003, 07:12:15
Job time : 33 secs

TELEFAX: (713) 799 2679
TELEX: 79-0924
INFORMATION FOR SEQ ID NO: 71
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-429-964-77

Query Match: 70.0%; Score 49; DB 2; Length 10;
Best Local Similarity: 100.0%; Pred. No. 0.0;
Matches: 10; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

QY 5 KKKKKSKTK 14
DB 1 KKKKKSKTK 10

RESULT 2
US-09-429-964-77
Sequence 73, Application US/08429964
Patent No. 5962243
GENERAL INFORMATION:
APPLICANT: BROWN, MICHAEL S.
APPLICANT: COLESTEIN, JESSIE L.
APPLICANT: PETER, VIVIAN
APPLICANT: JAMES, GUY L.
TITLE OF INVENTION: METHODS FOR THE IDENTIFICATION OF PEPTIDES
TITLE OF INVENTION: TRANSPEPTIDE INHIBITORS
NUMBER OF SEQUENCES: 85
CORRESPONDENCE ADDRESS:
ADDRESSER: APNOLD, WHITE & DURKEE
STREET: P.O. BOX 4433
CITY: HOUSTON
STATE: TEXAS
COUNTRY: UNITED STATES OF AMERICA
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
SOFTWARE: Patent In Release #1.0, Version #1.10
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/429,964
FILING DATE: 27-APR 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/021,825
FILING DATE: 16-FEB-1993
CLASSIFICATION: 435
APPLICATION NUMBER: US 07/820,011
FILING DATE: ABANDONED
CLASSIFICATION: 435
APPLICATION NUMBER: PTT/02/01/2000
FILING DATE: 19-APR 1991
CLASSIFICATION: 435
APPLICATION NUMBER: US 07/615,715
FILING DATE: 20-NOV 1990
CLASSIFICATION: 435
APPLICATION NUMBER: US 07/510,706
FILING DATE: 18-APR 1990 (ABANDONED)
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: PARKER, DAVID L.
REGISTRATION NUMBER: 30,165
REFERENCE/DOCKET NUMBER: US 07/410,749
TELEPHONE: (512) 418-3000
TELEFAX: (713) 789-2679
TELEX: 79-0924
INFORMATION FOR SEQ ID NO: 71

SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-429-964-73

Query Match: 70.0%; Score 49; DB 2; Length 14;
Best Local Similarity: 100.0%; Pred. No. 0.0;
Matches: 10; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

QY 5 KKKKKSKTK 14
DB 1 KKKKKSKTK 10

RESULT 3
US-08-584-043A-45
Sequence 45, Application US/08584043A
Patent No. 634436
GENERAL INFORMATION:
APPLICANT: Smith, Louis C.
APPLICANT: Sparrow, James T.
APPLICANT: Hauer, Jochen
APPLICANT: Mims, Martha P.
TITLE OF INVENTION: LIPOPHILIC PEPTIDES FOR
TITLE OF INVENTION: MATERNAL-FETAL DELIVERY
NUMBER OF SEQUENCES: 139
CORRESPONDENCE ADDRESS:
ADDRESSER: LYON & LYON
STREET: 633 West Fifth Street
SUITE: Suite 4700
CITY: LOS ANGELES
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 6.0
SOFTWARE: Word Perfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/584,043A
FILING DATE: January 9, 1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Waiburg, Richard J.
REGISTRATION NUMBER: 30,327
REFERENCE/DOCKET NUMBER: 21,189
TELECOMMUNICATION INFORMATION:
TELEPHONE: 413, 482 1600
TELEFAX: 4213, 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
OTHER INFORMATION: "Xaa" stands for any naturally
OTHER INFORMATION: occurring amino acid and
OTHER INFORMATION: analogues thereof.
US-08-584 043A 45

Query Match: 60.0%; Score 42; DB 4; Length 13;
Best Local Similarity: 67.2%; Pred. No. 3.3;


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ADDRESS: Lyon & Lyon
STREET: 633 West Fifth Street
SUITE: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 6.0
SOFTWARE: Word Perfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 844436
FILING DATE: January 8, 1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/POCKET NUMBER: 217/183
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-9510
INFORMATION FOR SEQ. IF NO. 44
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
OTHER INFORMATION: "Xaa" stands for any naturally
OTHER INFORMATION: occurring amino acid and
OTHER INFORMATION: analogues thereof.
US 08-584-043A-43

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Query Match 57.1%; Score 40; PP 4; Length 11;

Best Local Similarity 92.01; Freq No 5.74; Mismatches 0; Conservative 0; Gaps 0;

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QY 5 XXXXXSKY 14
    |||||
DB 2 XXXXXXXXX 11

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RESULT 7

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US-08-584-043A-44
Sequence 44, Application US-08-584-043A
Patent No. 6344436
GENERAL INFORMATION:
APPLICANT: Smith, Louis C.
APPLICANT: Sparrow, James T.
APPLICANT: Hauser, Jochen
APPLICANT: Mims, Martha P.
TITLE OF INVENTION: LIPOPHILIC PEPTIDES FOR
TITLE OF INVENTION: MACROMOLECULE DELIVERY
NUMBER OF SEQUENCES: 139
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
SUITE: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

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COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 6.0
SOFTWARE: Word Perfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 844436
FILING DATE: January 8, 1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/POCKET NUMBER: 217/183
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-9510
INFORMATION FOR SEQ. IF NO. 44
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
OTHER INFORMATION: "Xaa" stands for any naturally
OTHER INFORMATION: occurring amino acid and
OTHER INFORMATION: analogues thereof.
US-08-584-043A-44

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Query Match 57.1%; Score 40; PP 4; Length 12;

Best Local Similarity 92.01; Freq No 5.74; Mismatches 0; Conservative 0; Gaps 0;

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QY 5 XXXXXSKY 14
    |||||
DB 2 XXXXXXXXX 12

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RESULT 8

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US-08-584-043A-7
Sequence 7, Application US-08-584-043A
Patent No. 6344436
GENERAL INFORMATION:
APPLICANT: Smith, Louis C.
APPLICANT: Sparrow, James T.
APPLICANT: Hauser, Jochen
APPLICANT: Mims, Martha P.
TITLE OF INVENTION: LIPOPHILIC PEPTIDES FOR
TITLE OF INVENTION: MACROMOLECULE DELIVERY
NUMBER OF SEQUENCES: 139
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
SUITE: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 6.0
SOFTWARE: Word Perfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 844436
FILING DATE: January 8, 1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:

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Query Match
Best Local Similarity 57.13; Score 40; DB 4; Length 14;
Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QV 2 KGGKYYKYSYK 14
DB 1 KGGKYYKYSYK 13

RESULT 10
US-08-584-043A-8
Sequence 8, Application US/584043A
Patent No. 6344436

GENERAL INFORMATION:
APPLICANT: Smith, Louis C.
APPLICANT: Sparrow, James T.
APPLICANT: Hauser, Jocheen
APPLICANT: Mims, Martha P.
TITLE OF INVENTION: LIPOPHILIC PEPTIDES FOR
TITLE OF INVENTION: MACROMOLECULE DELIVERY
NUMBER OF SEQUENCES: 139
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 MB
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 6.0
SOFTWARE: Word Perfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/584,043A
FILING DATE: January 8, 1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:

ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 217/189
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1400
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-584-043A-8

Query Match
Best Local Similarity 57.13; Score 40; DB 4; Length 14;
Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QV 2 KGGKYYKYSYK 14
DB 2 KGGKYYKYSYK 14

RESULT 11
US-08-584-043A-102

Query Match
Best Local Similarity 57.13; Score 40; DB 4; Length 14;
Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QV 2 KGGKYYKYSYK 14
DB 1 KGGKYYKYSYK 13

RESULT 10
US-08-584-043A-8
Sequence 8, Application US/584043A
Patent No. 6344436

GENERAL INFORMATION:
APPLICANT: Smith, Louis C.
APPLICANT: Sparrow, James T.
APPLICANT: Hauser, Jocheen
APPLICANT: Mims, Martha P.
TITLE OF INVENTION: LIPOPHILIC PEPTIDES FOR
TITLE OF INVENTION: MACROMOLECULE DELIVERY
NUMBER OF SEQUENCES: 139
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 MB
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 6.0
SOFTWARE: Word Perfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/584,043A
FILING DATE: January 8, 1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:

ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 217/189
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1400
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-584-043A-8

Query Match
Best Local Similarity 57.13; Score 40; DB 4; Length 14;
Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QV 2 KGGKYYKYSYK 14
DB 2 KGGKYYKYSYK 14

RESULT 11
US-08-584-043A-102

? Sequence 102, Application US/8454043A
? Patent No. 5344436
? GENERAL INFORMATION:
? APPLICANT: Smith, Louis C.
? APPLICANT: Sparrow, James T.
? APPLICANT: Hauer, Jochee
? APPLICANT: Mims, Martha F.
? TITLE OF INVENTION: LIPOPHILIC PEPTIDES FOR
? TITLE OF INVENTION: MATERNAL-NEURON DELIVERY
? NUMBER OF SEQUENCES: 139
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Lyon & Lyon
? STREET: 633 West Fifth Street
? STREET: Suite 4700
? CITY: Los Angeles
? STATE: California
? COUNTRY: USA
? ZIP: 90011-2668
? COMPUTER READABLE FORM:
? MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
? MEDIUM TYPE: Storage
? COMPUTER: IBM Compatible
? OPERATING SYSTEM: IBM P.C. DOS 6.0
? SOFTWARE: Word Perfect 6.1
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/544,043A
? FILING DATE: January 8, 1992
? CLASSIFICATION: 435
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER:
? FILING DATE:
? ATTORNEY/AGENT INFORMATION:
? NAME: Warburg, Richard J.
? REGISTRATION NUMBER: 32,327
? REFERENCE/DOCKET NUMBER: 21/189
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (213) 489-1600
? TELEFAX: (213) 489-6440
? TELEX: 67-3510
? INFORMATION FOR SEQ ID NO: 102:
? SEQUENCE CHARACTERISTICS:
? LENGTH 14 amino acids
? TYPE: amino acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? MOLECULE TYPE: Peptide
? US-08-594-043A-102

Query Match 57.1%, Score 40, DB 4, Length 14,
Best Local Similarity 59.0%, Pred. No. 615,
Matches 9, Conservative 0, Mismatches 4, Indels 0, Gaps 0

QY ? KKKKKKKKKKKK 14
DB ? KKKKKKKKKKKK 14

RESULT 12
US-08-097-810E-1
? Sequence 1, Application US/8237810E
? Patent No. 5052211
? GENERAL INFORMATION:
? APPLICANT: Folio, Massimo
? TITLE OF INVENTION: Peptides for Neutralizing the
? TITLE OF INVENTION: Toxicity of Lipid A
? NUMBER OF SEQUENCES: 35
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Folio, Massimo & Costigan, James V.
? STREET: 1185 Avenue of the Americas
? CITY: New York
? STATE: New York
? COUNTRY: USA
? ZIP: 10016

? COMPUTER READABLE FORM:
? MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
? COMPUTER: IBM PS/2
? OPERATING SYSTEM: DOS
? SOFTWARE: Word Perfect 5.1
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/097,810E
? FILING DATE:
? CLASSIFICATION: 514
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER:
? FILING DATE:
? ATTORNEY/AGENT INFORMATION:
? NAME: Costigan, James V.
? REGISTRATION NUMBER: 25,669
? REFERENCE/DOCKET NUMBER: 576-004
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (212) 302-8998
? TELEFAX: (212) 302-8998
? INFORMATION FOR SEQ ID NO: 1:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 10 amino acids
? TYPE: amino acid
? US-08-097-810E-1

Query Match 55.7%, Score 29, DB 1, Length 10,
Best Local Similarity 60.0%, Pred. No. 67,
Matches 8, Conservative 0, Mismatches 2, Indels 0, Gaps 0

QY 5 KKKKKKKKKK 14
DB 1 KKKKKKKKKK 10

RESULT 13
US-08-456-112B-1
? Sequence 1, Application US/8444112B
? Patent No. 5344430
? GENERAL INFORMATION:
? APPLICANT: Folio, Massimo
? TITLE OF INVENTION: IDENTIFICATION OF ANTIHISTICS
? NUMBER OF SEQUENCES: 45
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Folio, Massimo & Costigan
? STREET: 1185 Avenue of the Americas
? CITY: New York
? STATE: New York
? COUNTRY: USA
? ZIP: 10016
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
? COMPUTER: LEADING EDGE 486
? OPERATING SYSTEM: DOS
? SOFTWARE: Word Perfect 5.1
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/456,112B
? FILING DATE: May 31, 1995
? CLASSIFICATION: 514
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER:
? FILING DATE:
? ATTORNEY/AGENT INFORMATION:
? NAME: Costigan, James V.
? REGISTRATION NUMBER: 25,669
? REFERENCE/DOCKET NUMBER: 576-004
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (212) 302-8998
? TELEFAX: (212) 302-8998
? INFORMATION FOR SEQ ID NO: 1:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 10 amino acids
? TYPE: amino acid

Sequence 100, Application US/08584043A

Patent No. 6344436

GENERAL INFORMATION:

APPLICANT: Smith, Louis C.

APPLICANT: Sparrow, James T.

APPLICANT: Hauer, Jochen

APPLICANT: Mims, Martha P.

TITLE OF INVENTION: LIPOPHILIC PEPTIDES FOR

MACROMOLECULE DELIVERY

TITLE OF INVENTION: MACROMOLECULE DELIVERY

NUMBER OF SEQUENCES: 139

CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon & Lyon

STREET: 633 West Fifth Street

CITY: Los Angeles

STATE: California

COUNTRY: U.S.A.

ZIP: 90071 2066

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

MEDIUM TYPE: storage

COMPUTER: IBM Compatible

OPERATING SYSTEM: IBM P.C. DOS 6.0

SOFTWARE: Word Perfect 6.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/584,043A

FILING DATE: January 8, 1996

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Warburg, Richard J.

REGISTRATION NUMBER: 32,327

REFERENCE/DOCKET NUMBER: 217/189

TELECOMMUNICATION INFORMATION:

TELEPHONE: (213) 489-1600

TELEFAX: (213) 955-0440

TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 100:

SEQUENCE CHARACTERISTICS:

LENGTH: 12 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MULTICLUF TYPE: peptide

US-08-584-043A-100

Query Match 55.7% Score 19; ID 4; Length 12

Best Local Similarity 80.0% Pred No. 7.84

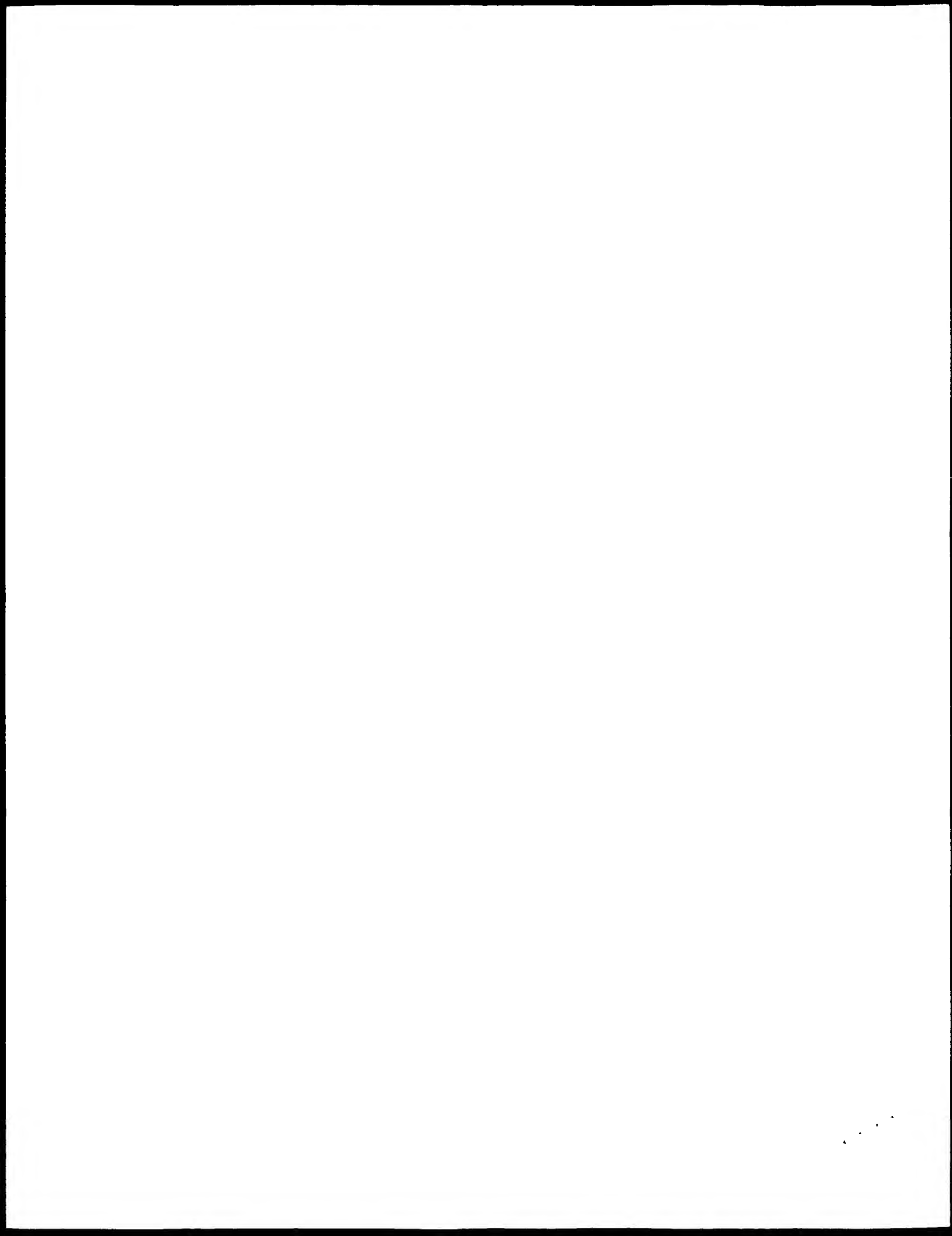
Matches 8; Conservative 0; Mismatches 2; Indels 1

QY 5 XXXXXXXXX 14

DB 1 XXXXXXXXX 10

Search completed: March 3, 2003, 07:05:29

Job time : 14 secs





Creation date: 09-17-2003
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1	NPL	10

Total number of pages: 10

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